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- (B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

AATGCGGCCA CTCCAAGGAG GCCGGGAGGA TTGTGGGAGG CCAAGACACC CAGGAAGGAC	60
GCTGGCCGTG GCAGGTGGC CTGTGGTTGA CCTCAGTGGG GCATGTATGT GGGGGCTCCC	120
TCATCCACCC ACGCTGGGTG CTCACAGCCG CCCACTGCTT CCTGAGGTCT GAGGATCCCG	180
GGCTCTACCA TGTTAAAGTC GGAGGGCTGA CACCCTCACT TTCAGAGCCC CACTCGGCCT	240
TGGTGGCTGT GAGGAGGCTC CTGGTCCACT CCTCATACCA TGGGACCACC ACCAGCGGGG	300
ACATTGCCCT GATGGAGCTG GACTCCCCCT TGCAGGCCTC CCAGTTCAGC CCCATCTGCC	360
TCCCAGGACC CCAGACCCCC CTCGCCATTG GGACCGTGTG CTGGGTAAAC GGGCTGGGGG	420
TCCACTCAGG AGAGGCCCTG GCGAGTGTC TTCAGGAGGT GGCTGTGCCC CTCCTGGACT	480
CGAACATGTG TGAGCTGATG TACCACCTAG GAGAGCCCAG CCTGGCTGGC CAGCGCCTCA	540
TCCAGGACGA CATGCTCTGT GCTGGCTCTG TCAGGGCAA GAAAGACTCC TGCCAGGGTG	600
ACTCCGGGGG GCCGCTGGTC TGCCCCATCA ATGATACGTG GATCCAGGCC GGCATTGTGA	660
GCTGGGGATT CCGCTGTGCC CGGCCTTTCC GGCCTGGTGT CTACACCCAG GTGCTAAGCT	720
ACACAGACTG GATTCAGAGA ACCCTGGCTG AATCTCACTC AGGCATGTCT GGGGCCCCGCC	780
CAGGTGCCCC AGGATCCCAC TCAGGCACCT CCAGATCCCA CCCAGTGCTG CTGCTTGAGC	840
TGTTGACCGT ATGCTTGCTT GGGTCCCTGT GAACCATGAG CCATGGAGTC CGGGATCCCC	900
TTTCTGGTAG GATTGATGGA ATCTAATAAT AAA	933

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 980 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CCTGTGGTCG	CCCCAGGATG	CTGAACCGAA	TGGTGGGCGG	GCAGGACACG	CAGGAGGGCG	60
AGTGGCCCTG	GCAAGTCAGC	ATCCAGCGCA	ACGGAAGCCA	CTTCTGCGGG	GGCAGCCTCA	120
TCGCGGAGCA	GTGGGTCTCG	ACGGCTGCGC	ACTGCTTCCG	CAACACCTCT	GAGACGTCCC	180
TGTACCAGGT	CCTGCTGGGG	GCAAGGCAGC	TAGTGCAGCC	GGGACCACAC	GCTATGTATG	240
CCCGGGTGAG	GCAGGTGGAG	AGCAACCCCC	TGTACCAGGG	CACGGCCTCC	AGCGTGACG	300
TGGCCCTGGT	GGAGCTGGAG	GCACCAGTGC	CCTTCACCAA	TTACATCCTC	CCCGTGTGCC	360
TGCCTGACCC	CTCGGTGATC	TTTGAGACGG	GCATGAACTG	CTGGGTCACT	GGCTGGGGCA	420
GCCCCAGTGA	GGAAGACCTC	CTGCCCCAAC	CGCGGATCCT	GCAGAAACTC	GCTGTGCCCA	480
TCATCGACAC	ACCCAAGTGC	AACCTGCTCT	ACAGCAAAGA	CACCGAGTTT	GGCTACCAAC	540
CCAAAACCAT	CAAGAATGAC	ATGCTGTGCG	CCGGCTTCGA	GGAGGGCAAG	AAGGATGCCT	600
GCAAGGGCGA	CTCGGGCGGC	CCCCTGGTGT	GCCTCGTGGG	TCAGTCGTGG	CTGCAGGCGG	660
GGGTGATCAG	CTGGGGTGAG	GGCTGTGCCC	GCCAGAACCG	CCCAGGTGTC	TACATCCGTG	720
TCACCGCCCA	CCACAACCTG	ATCCATCGGA	TCATCCCCAA	ACTGCAGTTC	CAGCCAGCGA	780
GGTTGGGCGG	CCAGAAGTGA	GACCCCCGGG	GCCAGGAGCC	CCTTGAGCAG	AGCTCTGCAC	840
CCAGCCTGCC	CGCCACACCC	ATCCTGCTGG	TCCTCCCAGC	GCTGCTGTTG	CACCTGTGAG	900
CCCCACCAGA	CTCATTTGTA	AATAGCGCTC	CTTCCTCCCC	TCTCAAATAC	CCTTATTTTA	960
TTTATGTTTC	TCCCAATAAA					980

CLAIMS:

1. An isolated proteinaceous molecule involved in or associated with regulation of cell activity and/or viability comprising a sequence of amino acids encoded by a nucleotide sequence, at least a portion of which, is capable of being amplified by polymerase chain reaction (PCR) using the following primers:

5' ACAGAATTCTGGGTIGTTIACIGCIGCICAYTG3' [SEQ ID NO:1]; and

5' ACAGAATTCA XIGGICCCIC/GT/AXTCICCC3' [SEQ ID NO:2];

or a complementary form of said primers.

2. An isolated proteinaceous molecule according to claim 1 wherein said molecule is a serine proteinase comprising an amino acid sequence substantially as set forth in SEQ ID NO:4 or an amino acid sequence having at least 50% similarity thereto.

3. An isolated proteinaceous molecule according to claim 1 wherein said molecule is a serine proteinase comprising an amino acid sequence substantially as set forth in SEQ ID NO:6 or an amino acid sequence having at least 50% similarity thereto.

4. An isolated proteinase molecule according to claim 1 wherein said molecule is a serine proteinase comprising an amino acid sequence substantially as set forth in SEQ ID NO:8 or an amino acid sequence having at least about 50% similarity thereto.

5. An isolated proteinaceous molecule according to claim 1 wherein said molecule is a serine proteinase comprising a sequence of amino acids encoded by a nucleotide sequence substantially as set forth in SEQ ID NO:3 or a nucleotide sequence having at least 50% similarity thereto or a nucleotide sequence capable of hybridising to the sequence set forth in SEQ ID NO:3 under low stringency conditions at 42°C.

6. An isolated proteinaceous molecule according to claim 1 wherein said molecule is a serine proteinase comprising a sequence of amino acids encoded by a nucleotide sequence substantially as set forth in SEQ ID NO:5 or a nucleotide sequence having at least 50% similarity thereto or a nucleotide sequence capable of hybridising to the sequence set forth in SEQ ID NO:5 under low stringency conditions at 42°C.
7. An isolated proteinaceous molecule according to claim 1 wherein said molecule is a serine proteinase comprising a sequence of amino acids encoded by a nucleotide sequence substantially as set forth in SEQ ID NO:7 or a nucleotide sequence having at least 50% similarity thereto or a nucleotide sequence capable of hybridising to the sequence set forth in SEQ ID NO:7 under low stringency conditions at 42°C.
8. An isolated proteinaceous molecule according to claim 1 wherein said molecule is a kinase comprising an amino acid sequence substantially as set forth in SEQ ID NO:10 or having 50% amino acid similarity thereto.
9. An isolated proteinaceous molecule according to claim 1 wherein said molecule is a kinase comprising an amino acid sequence encoded by a nucleotide sequence substantially as set forth in SEQ ID NO:9 or a nucleotide sequence having at least 50% similarity thereto or a nucleotide sequence capable of hybridising to the nucleotide sequence set forth in SEQ ID NO:9 under low stringency conditions at 42°C.
10. An isolated nucleic acid molecule encoding a polypeptide wherein at least a portion of said nucleic acid molecule is capable of being amplified by polymerase chain reaction (PCR) using the following primers:

5' ACAGAATTCTGGGTIGTACIGCIGCICAYTG3' [SEQ ID NO:1]; and

5'ACAGAATTCA XIGGICCCIC/C/GT/AXTCICCC3' [SEQ ID NO:2];

or a complementary form of said primers.

11. An isolated nucleic acid molecule according to claim 10 wherein said polypeptide is a serine proteinase comprising an amino acid sequence substantially as set forth in SEQ ID NO:4 or an amino acid sequence having at least 50% similarity thereto.
12. An isolated nucleic acid molecule according to claim 10 wherein said polypeptide is a serine proteinase comprising an amino acid sequence substantially as set forth in SEQ ID NO:6 or an amino acid sequence having at least 50% similarity thereto.
13. An isolated nucleic acid molecule according to claim 10 wherein said polypeptide is a serine proteinase comprising an amino acid sequence substantially as set forth in SEQ ID NO:8 or an amino acid sequence having at least about 50% similarity thereto.
14. An isolated nucleic acid molecule according to claim 10 comprising a sequence of nucleotides substantially as set forth in SEQ ID NO:3 or a nucleotide sequence having at least 50% similarity thereto or a nucleotide sequence capable of hybridising to the sequence set forth in SEQ ID NO:3 under low stringency conditions at 42°C.
15. An isolated nucleic acid molecule according to claim 10 comprising a sequence of nucleotides substantially as set forth in SEQ ID NO:5 or a nucleotide sequence having at least 50% similarity thereto or a nucleotide sequence capable of hybridising to the sequence set forth in SEQ ID NO:5 under low stringency conditions at 42°C.
16. An isolated nucleic acid molecule according to claim 10 comprising a sequence of nucleotides substantially as set forth in SEQ ID NO:7 or a nucleotide sequence having at least 50% similarity thereto or a nucleotide sequence capable of hybridising to the sequence set forth in SEQ ID NO:7 under low stringency conditions at 42°C.
17. An isolated nucleic acid molecule according to claim 10 wherein said polypeptide is a kinase comprising an amino acid sequence substantially as set forth in SEQ ID NO:10 or having 50% amino acid similarity thereto.

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18. An isolated nucleic acid molecule according to claim 17 comprising a sequence of nucleotides encoded by a nucleotide sequence substantially as set forth in SEQ ID NO:9 or a nucleotide sequence having at least 50% similarity thereto or a nucleotide sequence capable of hybridising to the nucleotide sequence set forth in SEQ ID NO:9 under low stringency conditions at 42°C.
19. An isolated serine proteinase encoded by a gene proximal to a cluster of genes of a mammalian chromosome.
20. An isolated serine proteinase according to claim 19 wherein the mammalian chromosome is human chromosome 16p13.3 or its equivalent in a non-human species.
21. An isolated serine proteinase according to claim 20 wherein the gene cluster includes at least two genes having the nucleotide sequence as set forth in SEQ ID NO:3 or 5 or 28 or 29 or 30 or a nucleotide sequence having at least 50% similarity to any one of SEQ ID NO:3 or 5 or 28 or 29 or 30 or a nucleotide sequence capable of hybridizing to any one of the sequences under low stringency conditions at 42°C.
22. An isolated serine proteinase according to claim 20 wherein said serine proteinase is a short form of HELA2 having an amino acid sequence substantially as set forth in SEQ ID NO:4 or an amino acid sequence having at least 50% similarity thereto.
23. An isolated serine proteinase according to claim 20 wherein said serine proteinase is a long form of HELA2 having an amino acid sequence substantially as set forth in SEQ ID NO:6 or an amino acid sequence having at least 50% similarity thereto.
24. An isolated serine proteinase according to claim 22 encoded by a nucleotide sequence substantially as set forth in SEQ ID NO:3 or a nucleotide sequence having at least 50% similarity thereto or a sequence capable of hybridizing to SEQ ID NO:3 under low stringency conditions at 42°C.

25. An isolated serine proteinase according to claim 23 encoded by a nucleotide sequence substantially as set forth in SEQ ID NO:5 or a nucleotide sequence having at least 50% similarity thereto or a sequence capable of hybridizing to SEQ ID NO:5 under low stringency conditions at 42°C.
26. An isolated nucleic acid molecule comprising a nucleotide sequence encoding a serine proteinase and corresponding to a gene proximal to a cluster of genes encoding serine proteinases.
27. An isolated nucleic acid molecule according to claim 26 wherein the gene cluster includes at least two genes having the nucleotide sequence as set forth in SEQ ID NO:3 or 5 or 28 or 29 or 30 or a nucleotide sequence having at least 50% similarity to any one of SEQ ID NO:3 or 5 or 28 or 29 or 30 or a nucleotide sequence capable of hybridizing to any one of the sequences under low stringency conditions at 42°C.
28. An isolated nucleic acid molecule according to claim 25 comprising a nucleotide sequence substantially as set forth in SEQ ID NO:3 or SEQ ID NO:5 or a nucleotide sequence having at least about 50% similarity to either of SEQ ID NO:3 or SEQ ID NO:5 or a nucleotide sequence capable of hybridizing to SEQ ID NO:3 or SEQ ID NO:5 under low stringency conditions at 42°C.
29. An isolated kinase comprising an amino acid sequence substantially as set forth in SEQ ID NO:10 or an amino acid sequence having at least about 50% similarity thereto.
30. An isolated kinase according to claim 29 encoded by a nucleotide sequence substantially as set forth in SEQ ID NO:9 or a nucleotide sequence having at least 50% similarity thereto or capable of hybridizing to SEQ ID NO:9 under low stringency conditions at 42°C.
31. A method of regulating cell activity and/or viability said method comprising contacting said cell with an activity and/or viability effective amount of a serine proteinase and/or kinase.

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32. A method according to claim 31 wherein the serine proteinase comprises a sequence of amino acids encoded by a nucleotide sequence, at least a portion of which, is capable of being amplified by polymerase chain reaction (PCR) using the following primers:

5' ACAGAATTCTGGGTIGTTIACIGCIGCICAYTG3' [SEQ ID NO:1]; and

5'ACAGAATTCA XIGGICCCIC/GT/AXTCICCC3' [SEQ ID NO:2];

or a complementary form of said primers.

33. A method according to claim 31 wherein the serine proteinase comprises an amino acid sequence substantially as set forth in SEQ ID NO:4 or an amino acid sequence having at least 50% similarity thereto.

34. A method according to claim 31 wherein the serine proteinase comprises an amino acid sequence substantially as set forth in SEQ ID NO:6 or an amino acid sequence having at least 50% similarity thereto.

35. A method according to claim 31 wherein the serine proteinase comprises an amino acid sequence substantially as set forth in SEQ ID NO:8 or an amino acid sequence having at least about 50% similarity thereto.

36. A method according to claim 31 wherein the serine proteinase comprises a sequence of amino acids encoded by a nucleotide sequence substantially as set forth in SEQ ID NO:3 or a nucleotide sequence capable of hybridising to the sequence set forth in SEQ ID NO:3 under low stringency conditions at 42°C.

37. A method according to claim 31 wherein the serine proteinase comprises a sequence of amino acids encoded by a nucleotide sequence substantially as set forth in SEQ ID NO:5 or a nucleotide sequence having at least 50% similarity thereto or a nucleotide sequence capable of hybridising to the sequence set forth in SEQ ID NO:5 under low stringency conditions at 42°C.

38. A method according to claim 31 wherein the serine proteinase comprises a sequence of amino acids encoded by a nucleotide sequence substantially as set forth in SEQ ID NO:7 or a nucleotide sequence having at least 50% similarity thereto or a nucleotide sequence capable of hybridising to the sequence set forth in SEQ ID NO:7 under low stringency conditions at 42°C.
39. A method according to claim 31 wherein the kinase comprises an amino acid sequence substantially as set forth in SEQ ID NO:10 or having 50% amino acid similarity thereto.
40. A method according to claim 31 wherein the kinase comprises an amino acid sequence encoded by a nucleotide sequence substantially as set forth in SEQ ID NO:9 or a nucleotide sequence having at least 50% similarity thereto or a nucleotide sequence capable of hybridising to the nucleotide sequence set forth in SEQ ID NO:9 under low stringency conditions at 42°C.
41. A method of modulating fertility in a mammal said method comprising modulating levels of HELA2 wherein increasing levels of HELA2 facilitates sperm maturation and development.
42. A method according to claim 41 wherein fertility is enhanced by introducing recombinant HELA2.
43. A method according to claim 41 wherein fertility is reduced by down regulating expression of the HELA2 gene.
44. A composition comprising a serine proteinase and/or kinase capable of regulating cell activity and/or viability and one or more pharmaceutically acceptable carriers and/or diluents.
45. A composition according to claim 44 wherein the serine proteinase is HELA2 or a functional derivative thereof.
46. An isolated antibody capable of interacting with a proteinaceous molecule involved in or associated with regulation of cell activity and/or viability comprising a sequence of amino acids encoded by a nucleotide sequence, at least a portion of which, is capable of being

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amplified by polymerase chain reaction (PCR) using the following primers:

5' ACAGAATTCTGGGTIGTGTACIGCIGCICAYTG3' [SEQ ID NO:1]; and

5' ACAGAATTTCAXIGGICCCIC/GT/AXTCICC3' [SEQ ID NO:2];

or a complementary form of said primers.

47. An isolated antibody according to claim 46 wherein said proteinaceous molecule is a serine proteinase comprising an amino acid sequence substantially as set forth in SEQ ID NO:4 or an amino acid sequence having at least 50% similarity thereto.

48. An isolated antibody according to claim 46 wherein said proteinaceous molecule is a serine proteinase comprising an amino acid sequence substantially as set forth in SEQ ID NO:6 or an amino acid sequence having at least 50% similarity thereto.

49. An isolated antibody according to claim 46 wherein said proteinaceous molecule is a serine proteinase comprising an amino acid sequence substantially as set forth in SEQ ID NO:8 or an amino acid sequence having at least about 50% similarity thereto.

50. An isolated antibody according to claim 46 wherein said proteinaceous molecule is a serine proteinase comprising a sequence of amino acids encoded by a nucleotide sequence substantially as set forth in SEQ ID NO:3 or a nucleotide sequence having at least 50% similarity thereto or a nucleotide sequence capable of hybridising to the sequence set forth in SEQ ID NO:3 under low stringency conditions at 42°C.

51. An isolated antibody according to claim 46 wherein said proteinaceous molecule is a serine proteinase comprising a sequence of amino acids encoded by a nucleotide sequence substantially as set forth in SEQ ID NO:5 or a nucleotide sequence having at least 50% similarity thereto or a nucleotide sequence capable of hybridising to the sequence set forth in SEQ ID NO:5 under low stringency conditions at 42°C.

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52. An isolated antibody according to claim 46 wherein said proteinaceous said molecule is a serine proteinase comprising a sequence of amino acids encoded by a nucleotide sequence substantially as set forth in SEQ ID NO:7 or a nucleotide sequence having at least 50% similarity thereto or a nucleotide sequence capable of hybridising to the sequence set forth in SEQ ID NO:7 under low stringency conditions at 42°C.

53. An isolated antibody according to claim 46 wherein said proteinaceous molecule is a kinase comprising an amino acid sequence substantially as set forth in SEQ ID NO:10 or having 50% amino acid similarity thereto.

54. An isolated antibody according to claim 46 wherein said proteinaceous molecule is a kinase comprising an amino acid sequence encoded by a nucleotide sequence substantially as set forth in SEQ ID NO:9 or a nucleotide sequence having at least 50% similarity thereto or a nucleotide sequence capable of hybridising to the nucleotide sequence set forth in SEQ ID NO:9 under low stringency conditions at 42°C.

55. An antagonist or agonist to the isolated proteinaceous molecule according to any one of claims 1 to 9.

56. A method of determining a predisposition for or the presence of a cancer, said method comprising determining the presence of a nucleotide sequence encoding a proteinaceous molecule according to any one of claims 1 to 9.

57. A method according to claim 56 wherein the nucleotide sequence encodes a polypeptide wherein at least a portion of said nucleotide sequence is capable of being amplified by polymerase chain reaction (PCR) using the following primers:

5' ACAGAATTCTGGGTIGTIACIGCIGCICAYTG3' [SEQ ID NO:1]; and

5' ACAGAATTCA XIGGICCCIC/GT/AXTCICCC3' [SEQ ID NO:2];

or a complementary form of said primers.

58. A method according to claim 57 wherein said nucleotide sequence encodes a serine proteinase comprising an amino acid sequence substantially as set forth in SEQ ID NO:4 or an amino acid sequence having at least 50% similarity thereto.

59. A method according to claim 57 wherein said nucleotide sequence encodes a serine proteinase comprising an amino acid sequence substantially as set forth in SEQ ID NO:6 or an amino acid sequence having at least 50% similarity thereto.

60. A method according to claim 57 wherein said nucleotide sequence encodes a serine proteinase comprising an amino acid sequence substantially as set forth in SEQ ID NO:8 or an amino acid sequence having at least about 50% similarity thereto.

61. A method according to claim 57 wherein said nucleotide sequence is as substantially set forth in SEQ ID NO:3 or is a nucleotide sequence having at least 50% similarity thereto or a nucleotide sequence capable of hybridising to the sequence set forth in SEQ ID NO:3 under low stringency conditions at 42°C.

62. A method according to claim 57 wherein said nucleotide sequence is as substantially set forth in SEQ ID NO:5 or a nucleotide sequence having at least 50% similarity thereto or a nucleotide sequence capable of hybridising to the sequence set forth in SEQ ID NO:5 under low stringency conditions at 42°C.

63. A method according to claim 57 wherein said nucleotide sequence is as substantially set forth in SEQ ID NO:7 or a nucleotide sequence having at least 50% similarity thereto or a nucleotide sequence capable of hybridising to the sequence set forth in SEQ ID NO:7 under low stringency conditions at 42°C.

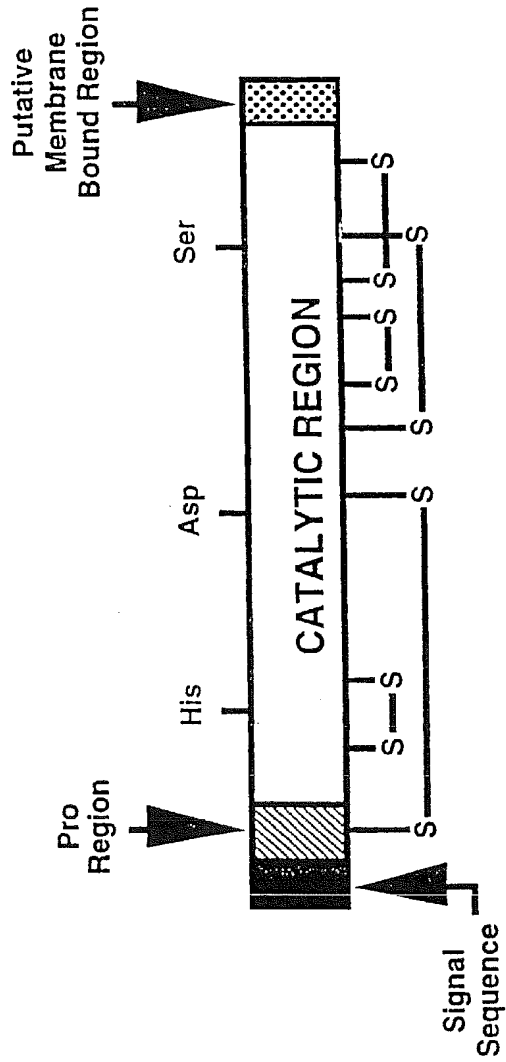
64. A method according to claim 57 wherein said nucleotide sequence is as substantially set forth in SEQ ID NO:10 or having 50% amino acid similarity thereto.

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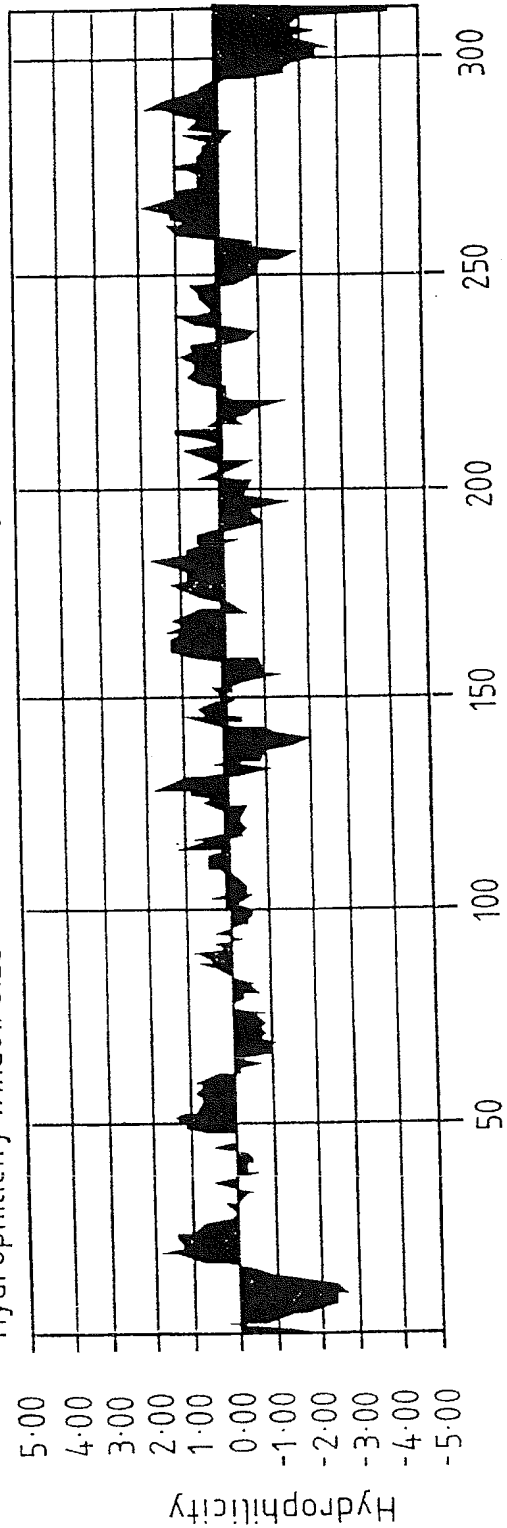
65. A method according to claim 57 wherein said nucleotide sequence is as substantially set forth in SEQ ID NO:9 or a nucleotide sequence having at least 50% similarity thereto or a nucleotide sequence capable of hybridising to the nucleotide sequence set forth in SEQ ID NO:9 under low stringency conditions at 42°C.

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FIG 1

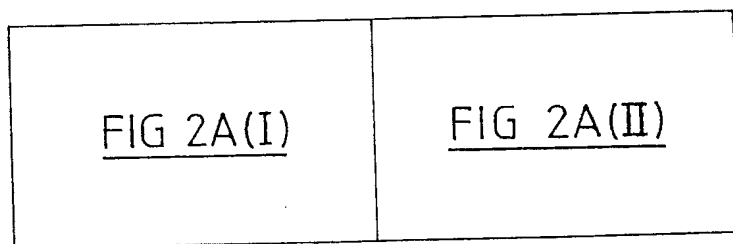


Hydrophobicity Window Size = 10 Scale = Kyte - Doolittle



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FIG 2A



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Sequence comparison of HELA2(Testisin) and prostatin

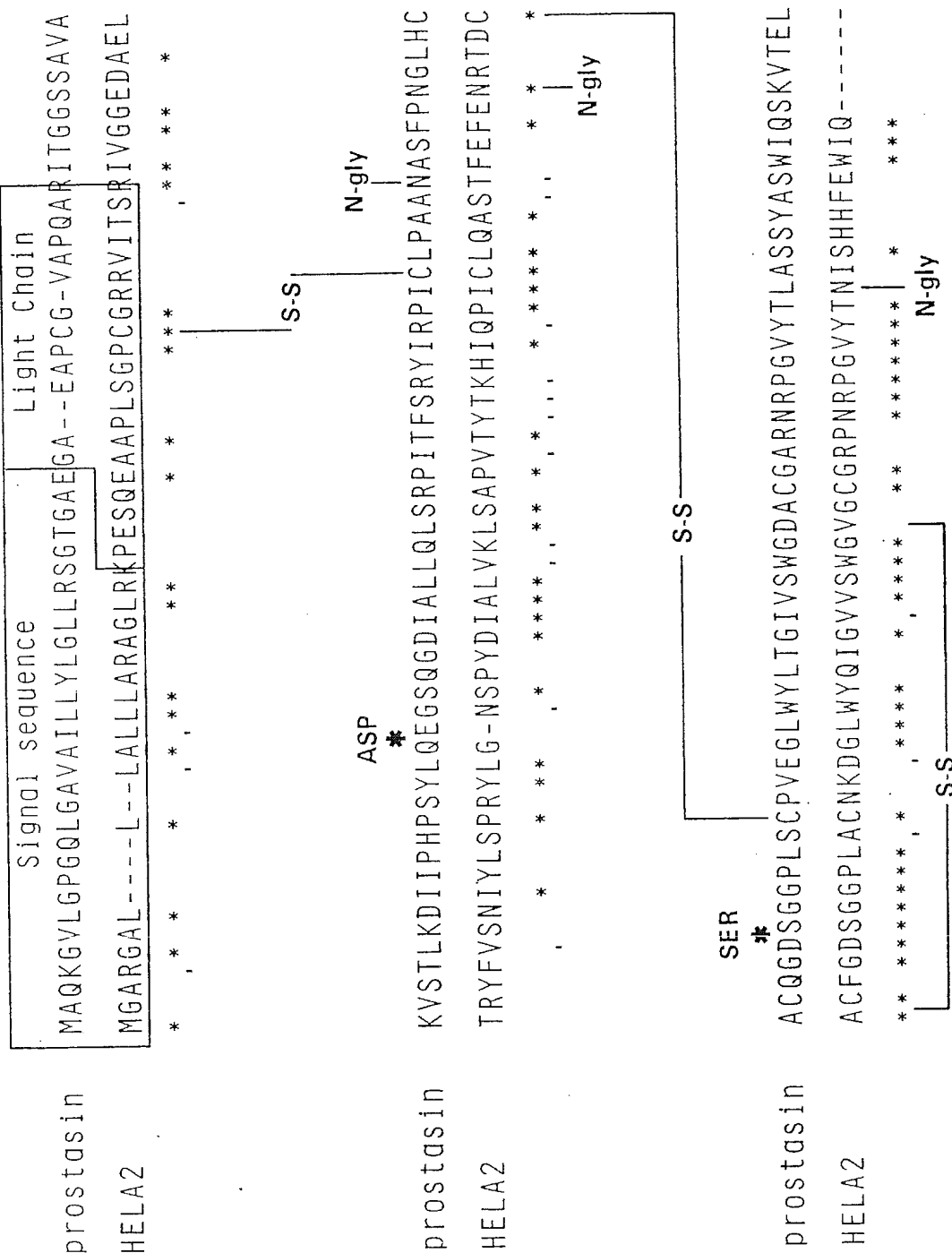


FIG 2A(I)

SH

✱

HELA2
GRWPWGSLRLWDSHVCVSLLSHRWALIAAHCFEIDLSDPSGWMMVQFGQLISITSIWCEGR

[illegible]/YS/
(Long)

(Long Isoform)

Heavy Chain

prostatic
TVTGWGHVAPSVSLTPKPLQQLEVPPLISRETCNCLYNIDAKPEEPHFVQEDMVCAGYVEGGND

HELA2
WVTGWGYIKEDEALPSHTLQEVQVAIIINNSMCNHLFLKYSFRKD--IFG-DMVCAGNAGGQGD

* * *

- - -

N-gly

55

Putative
Transmembrane
Domain

PILFLPLGLALGLLSPWL
PLLFFFPLLWALPLLGPV

* * * * *

HES

proctasin
QPRVVPQTQESQPDNLGSHLAFSSAPAQGLLR

HEL42
--KLMAQSGMSQPD-----PS---W

*
*
*
*
*

FIG 2A(II)

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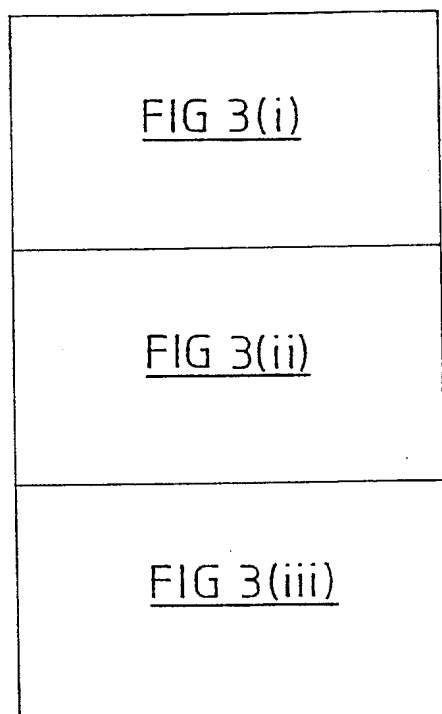
FIG 2B

In vitro transcription /
translation of HELA2 (Testisin)

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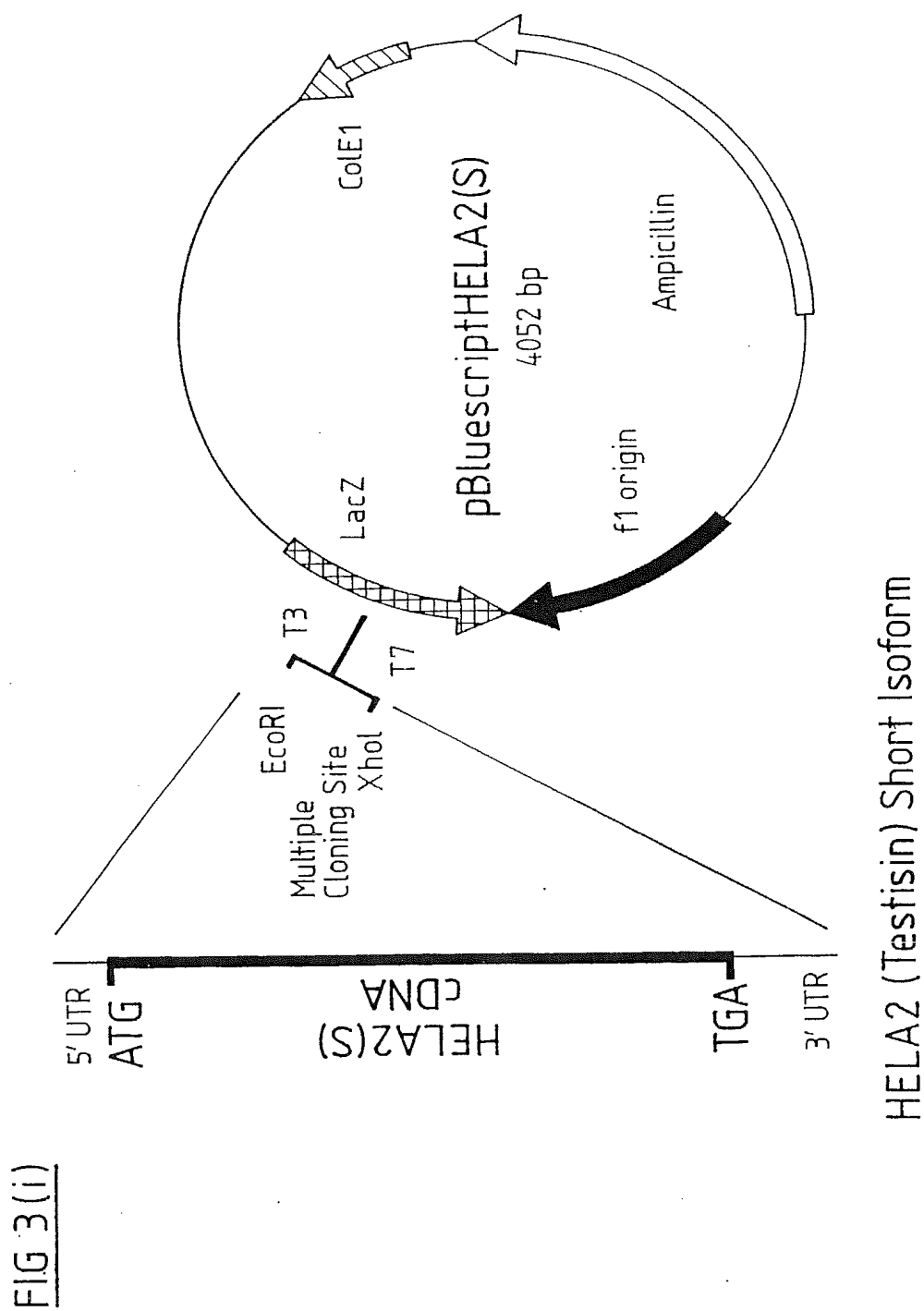
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FIG 3



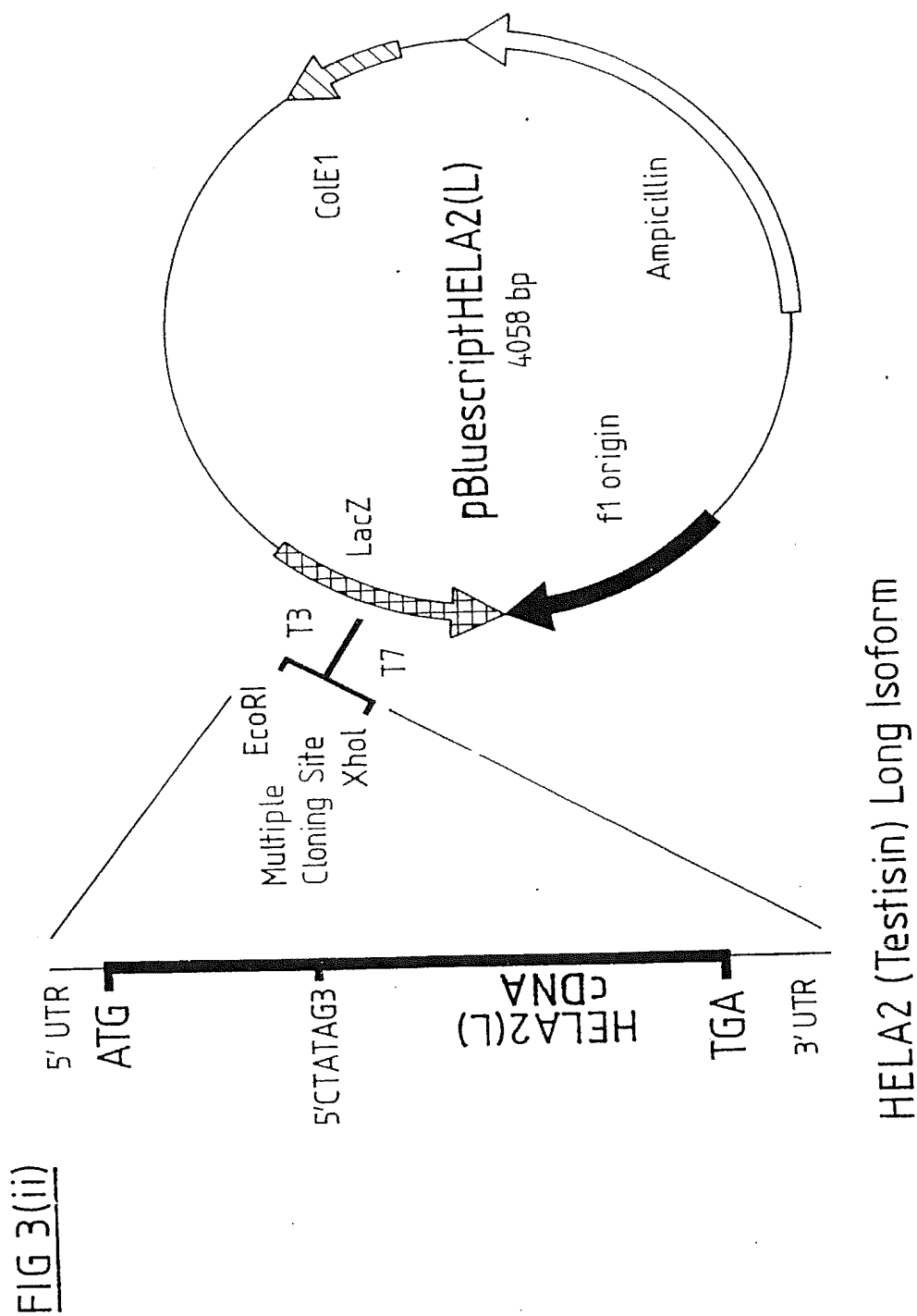
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HELA2 (Testisin) Restriction Enzyme Map

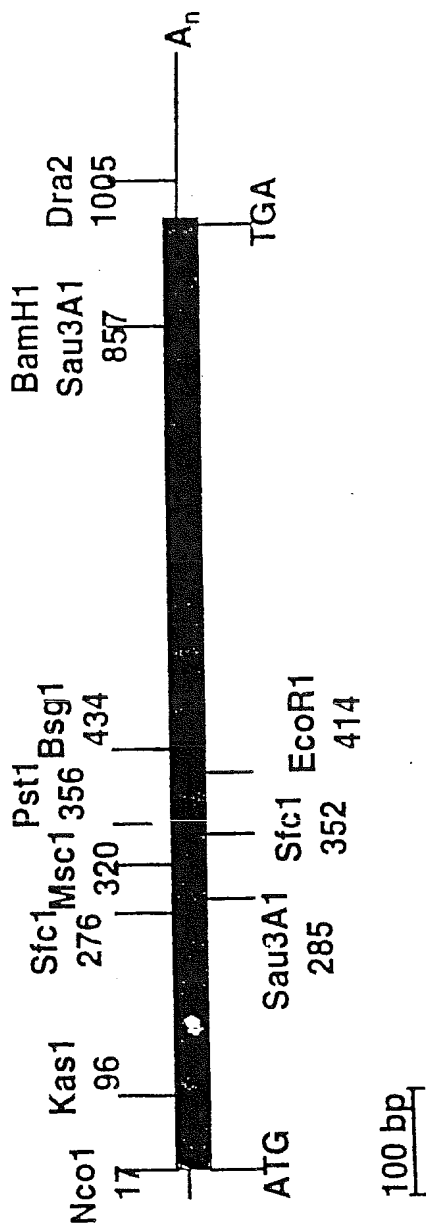
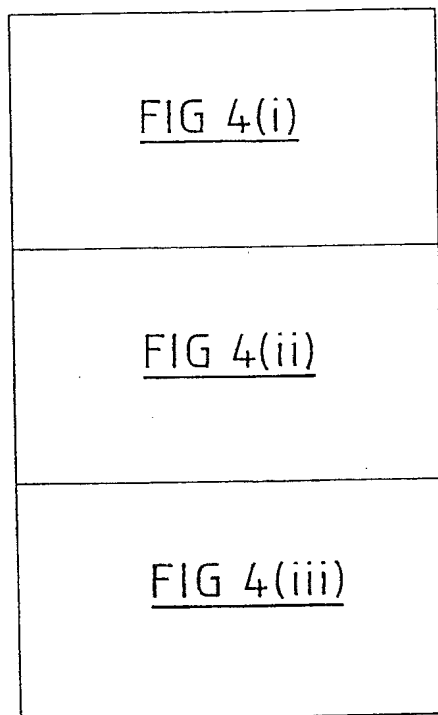


FIG 3(iii)

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FIG 4



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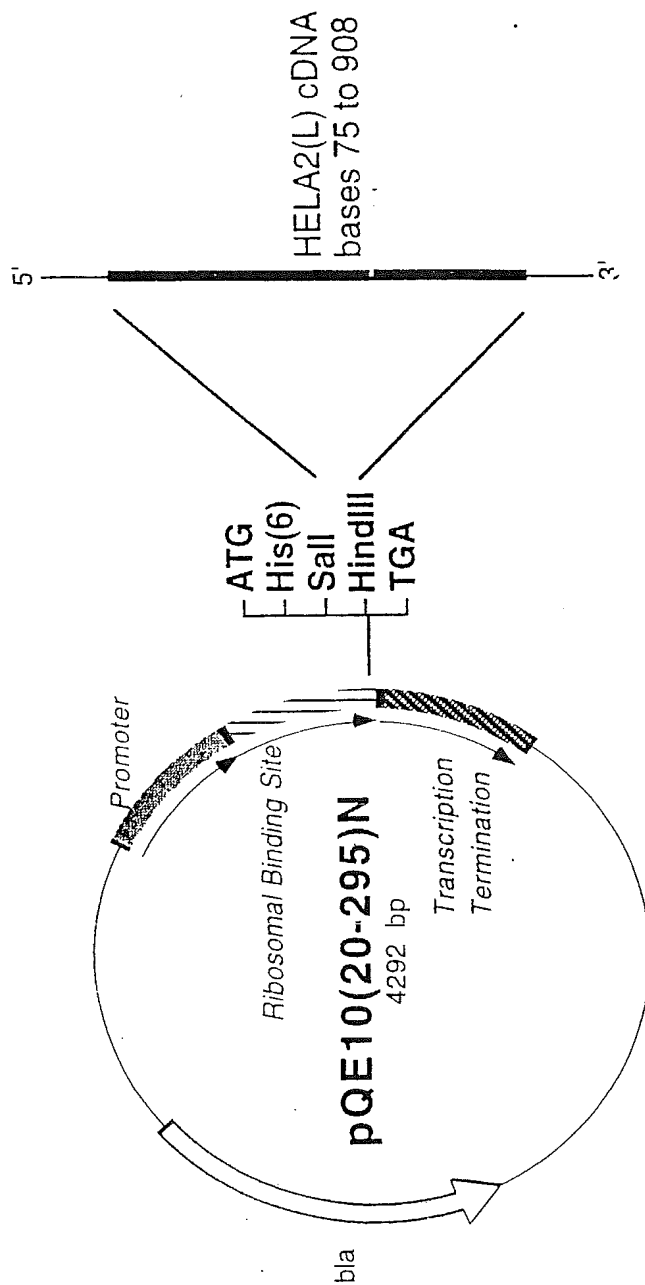


FIG 4(i)

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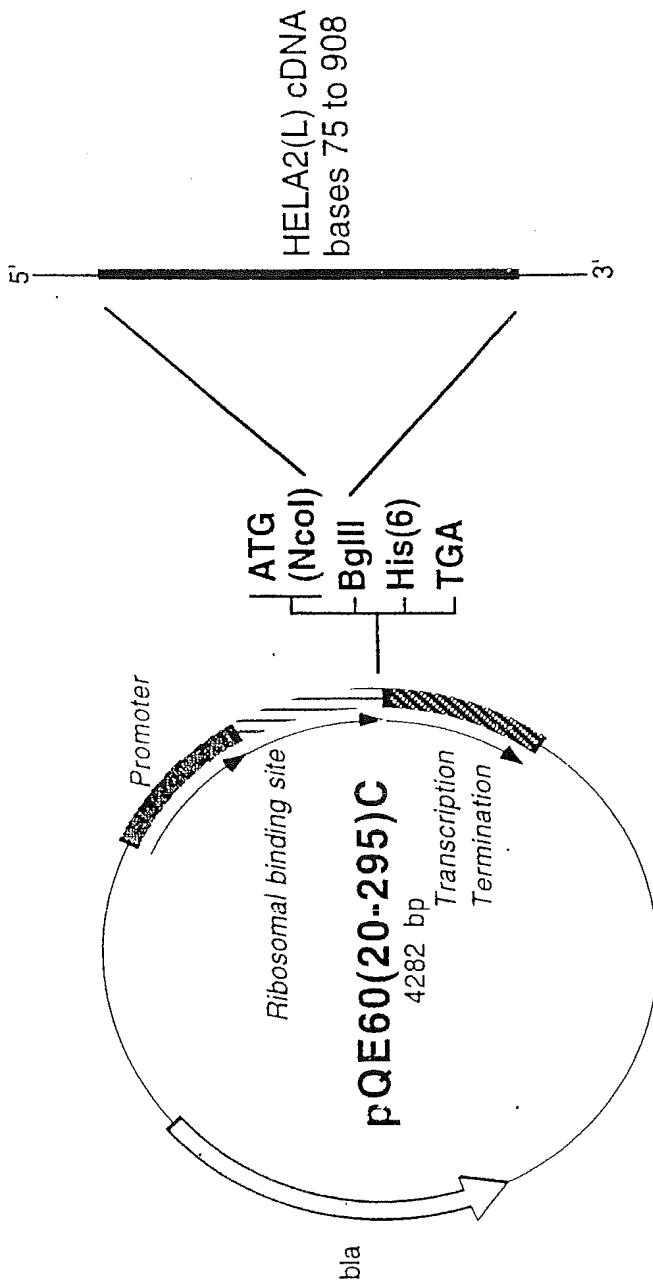


FIG 4(ii)

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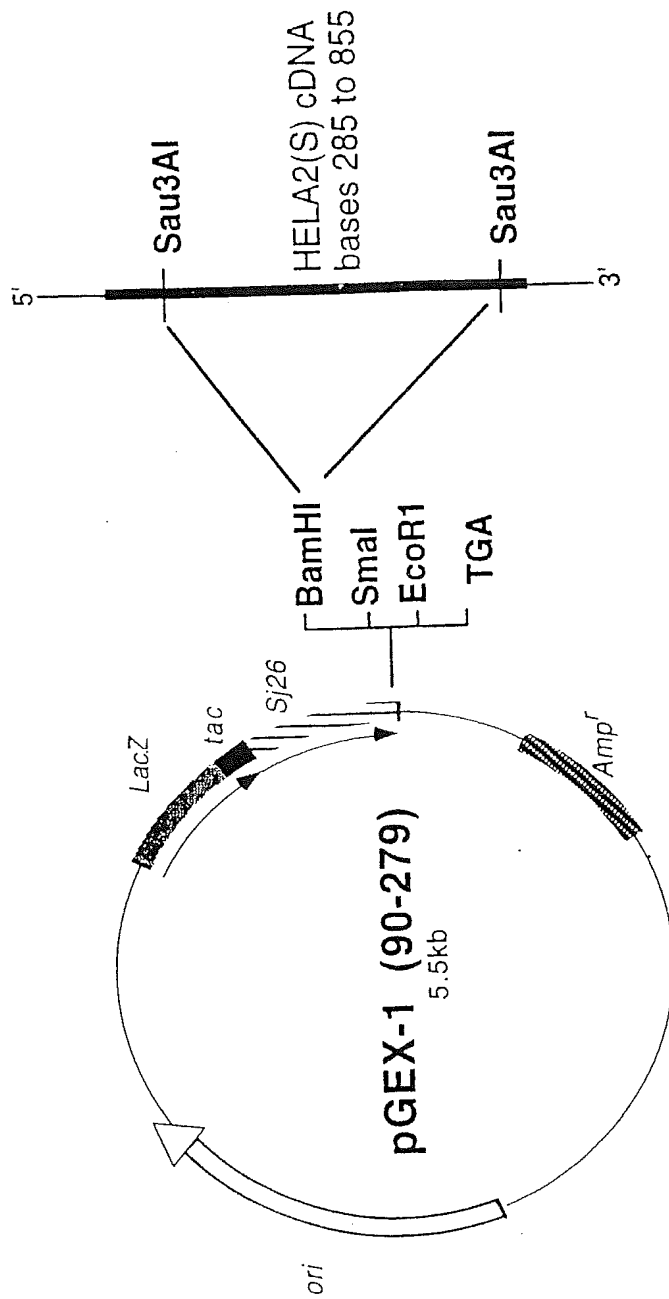
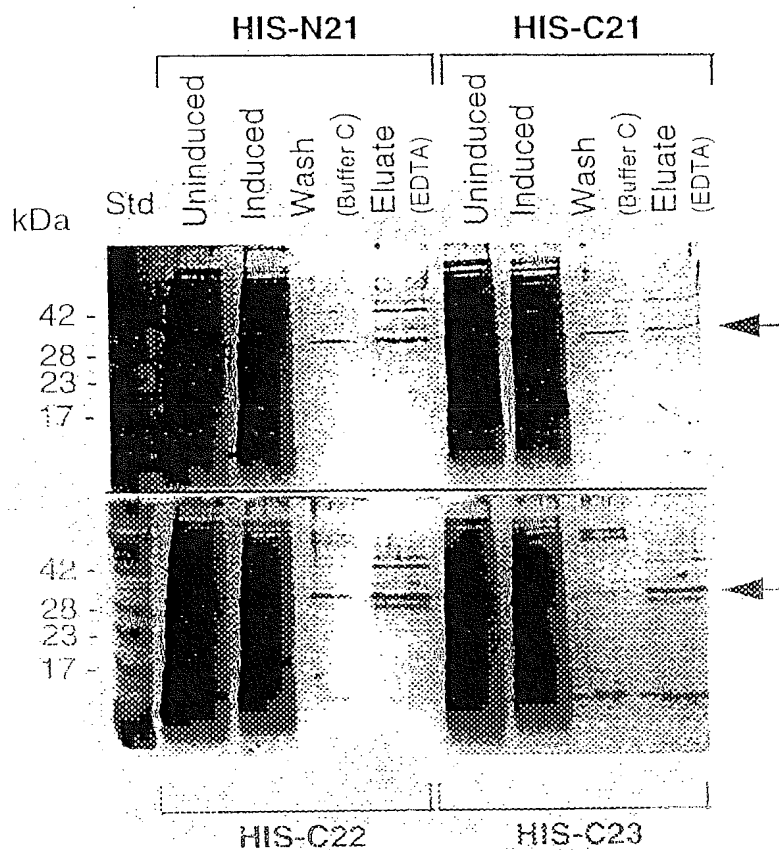
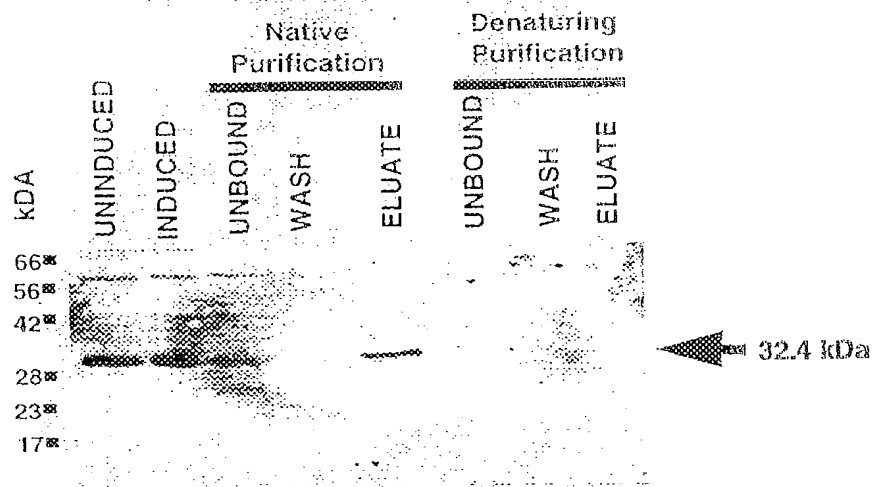


FIG 4(iii)

FIG 5

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A. Expression of recombinant Testisin in *E. coli*.**B. Western blot of recombinant Testisin**

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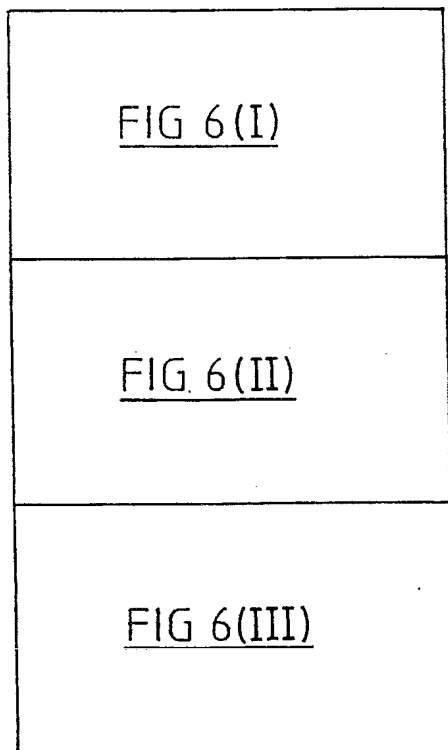


FIG 6

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FIGURE 6 (I)

1	GCCGCGGAGAGAGGCC	
119	ATGGCGCGCGGGCGCTGCTGCTGGCGCTGCTGGCTGGCTCAGGAAG	
	M G A R G A L L L A L L A R A G L R K	20
179	CCGAGTCGAGGAGCGCGCGTTATCAGGACCATGCGGCCGAGGGTCAACGTCG	
	P E S Q E A A P L S G P C G R R V I T S	40
1139	CGCATCGTGGTGAGAGACGCCGAACCTCGGGCGTTGGCCGTGGCAGGGAGCCTGCGC	
	R I V G G E D A E L G R W P W Q G S L R	60
1199	CTGTGGGATTCCCACGTATCGGGAGTGAGCCTGCTCAGCCACCCTGGGCACCTCACGGCG	
	L W D S H V C G V S L L S H R W A L T A	80
1259	GCGCACTGCTTTGAAACCTATAGTGACCTTAGTGATCCCTCCGGGTGGATGGTCCAGTTT	
	A H C F E T Y S D L S D P S G W M V Q F	100
1319	GGCAGCTGACTTCCATGCCATCCTTCTGGAGCCTGCAGGCCTACTACACCCGTTACTTC	
	G Q L T S M P S F W S L Q A Y Y T R Y F	120
1379	GTATCGAATATCTATCTGAGCCCTCGCTACCTGGGGAATTCACCCCTATGACATTGCCTTG	
	V S N I Y L S P R Y L G N S P Y D I A L	140

FIGURE 6 (II)

439 GTGAAGCTGTCTGCACCTGTACCTACACTAAACACATCCAGCCCATCTGTCTCCAGGCC
V K L S A P V T Y T K H I Q P I C L Q A 160

499 TCCACATTTGAGTTGAGAACCGGACAGACTGCTGGTGACTGGCTGGGGTACATCAAA
S T F E F E N R T D C W V T G W G Y I K 180

559 GAGGATGAGGCACTGCCATCTCCCCACACCCCTCCAGGAAGTTCAGGTCGCCATCATAAAC
E D E A L P S P H T L Q E V Q V A I I N 200

619 AACTCTATGTGCAACCACCTCTTCCCTCAAGTACAGTTTCCGCAAGGACATCTTTGGAGAC
N S M C N H L F L K Y S F R K D I F G D 220

679 ATGGTTTGTGCGCAATGCCCAAGCGGGAAGGATGCCCTGCTTCGGTGACTCAGGTGGA
M V C A G N A Q G G K D A C F G D S G G 240

739 CCCTTGGCCTGTAAACAAGAAATGGACTGTGTTATCAGATTGGAGTCGTGAGCTGGGGAGTG
P L A C N K N G L W Y Q I G V V S W G V 260

799 GGCTGTGGTCGGCCCAATCGGCCCGGTGTCTACACCAATATCAGCCACCACCTTGAGTGG
G C G R P N R P G V Y T N I S H H F E W 280

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FIGURE 6 (III)

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859 ATCCAGAAAGCTGATGGCCCAAGAGTGGCATGTCCAGCCAGACCCCTCCTGGCCGCTACTC
    I Q K L M A Q S G M S Q P D P S W P L L 300
919 TTTTTCCTCTTCTCTGGGCTCTCCCACTCCTGGGGCCGGTCTGAGCCTACCTGAGCCCA 314
    F F P L L W A L P L L G P V *
979 TGCAGCCTGGGGCCACTGCCAAGTCAGGCCCTGGTTCTCTCTTGTGTTGGTAATAA
1039 ACACATTCCAGTTGATGCCCTTGCAGGGCATTCTCAAAAAAATAAAAAAATAAAAAA
1099 AAAAAAAAAAAAAAAAAA
```

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Western blot of GST-Testisin using anti-Testisin peptide T175 antibody

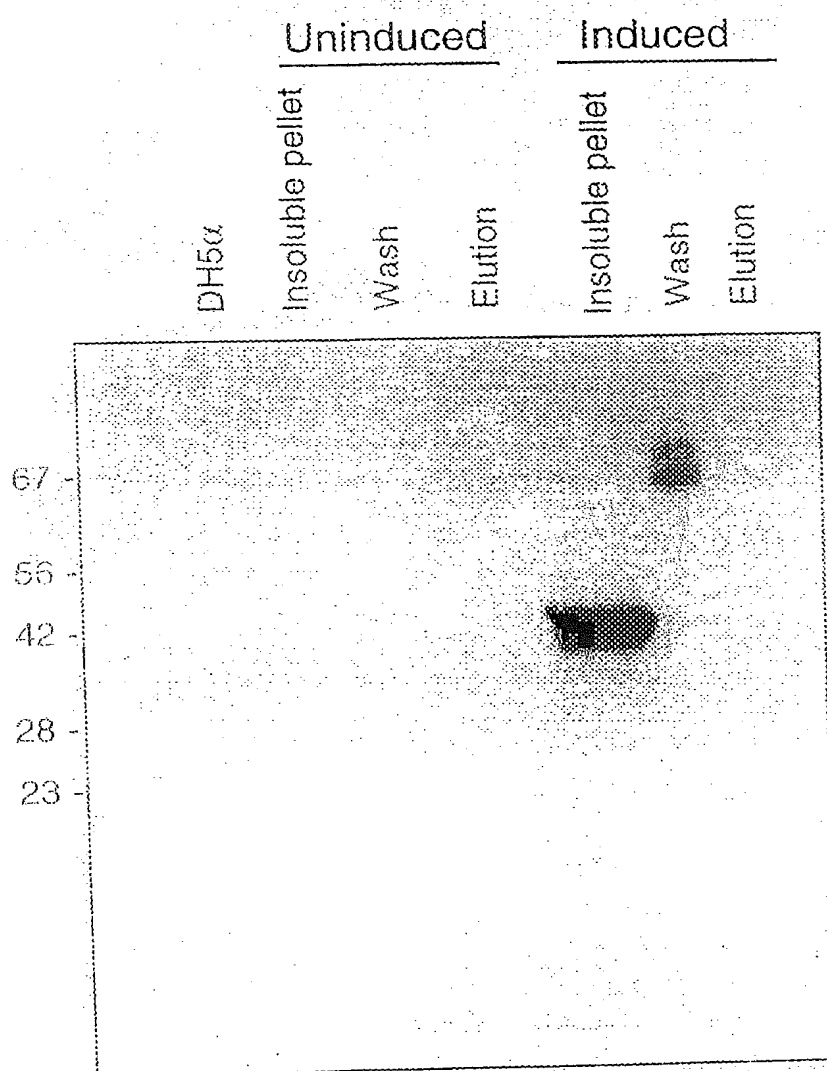
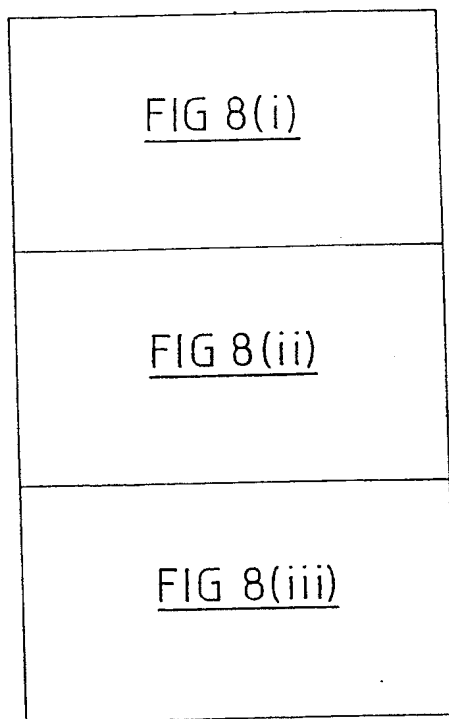


FIG 7

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FIG 8



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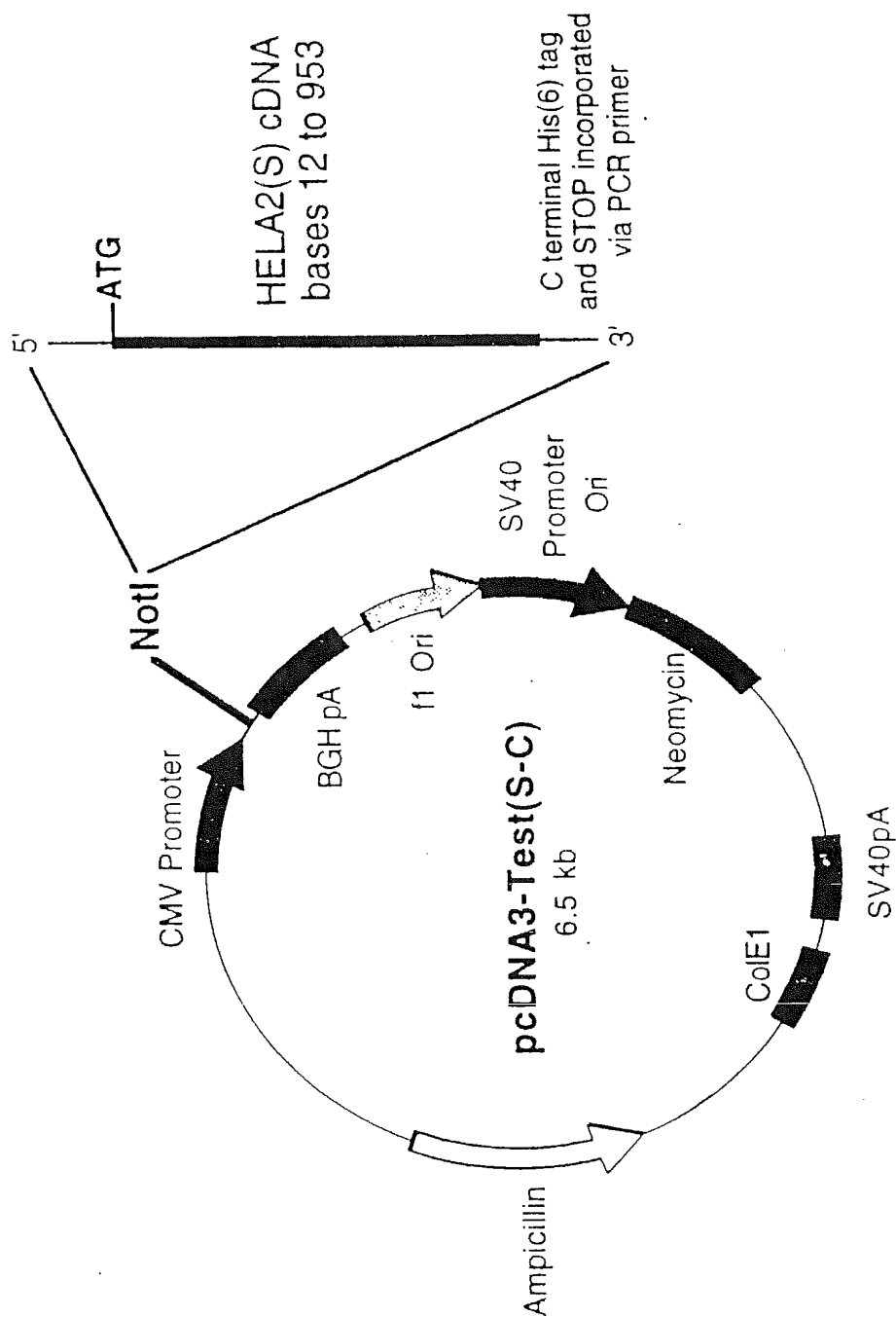


FIG 8(i)

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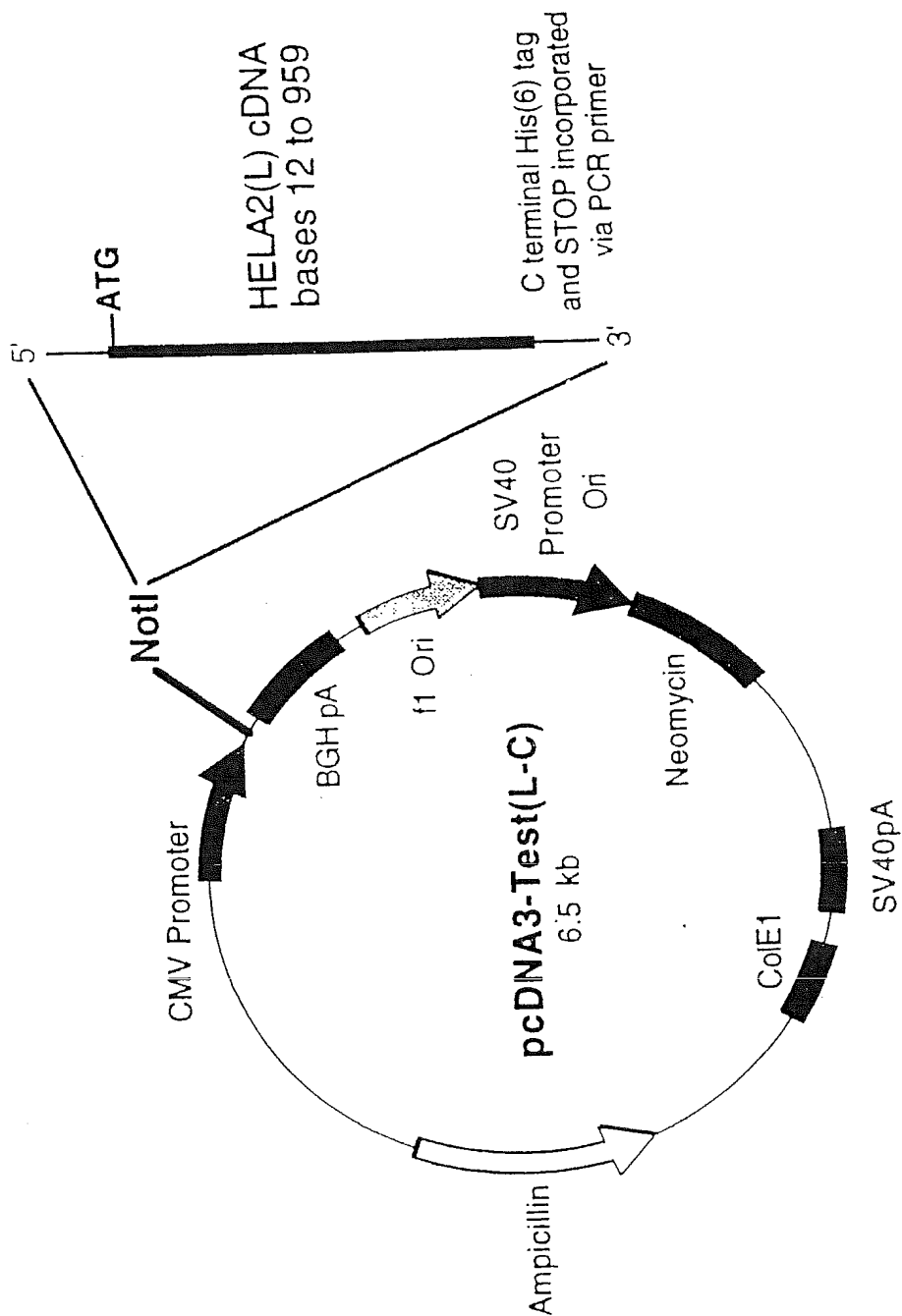


FIG 8(ii)

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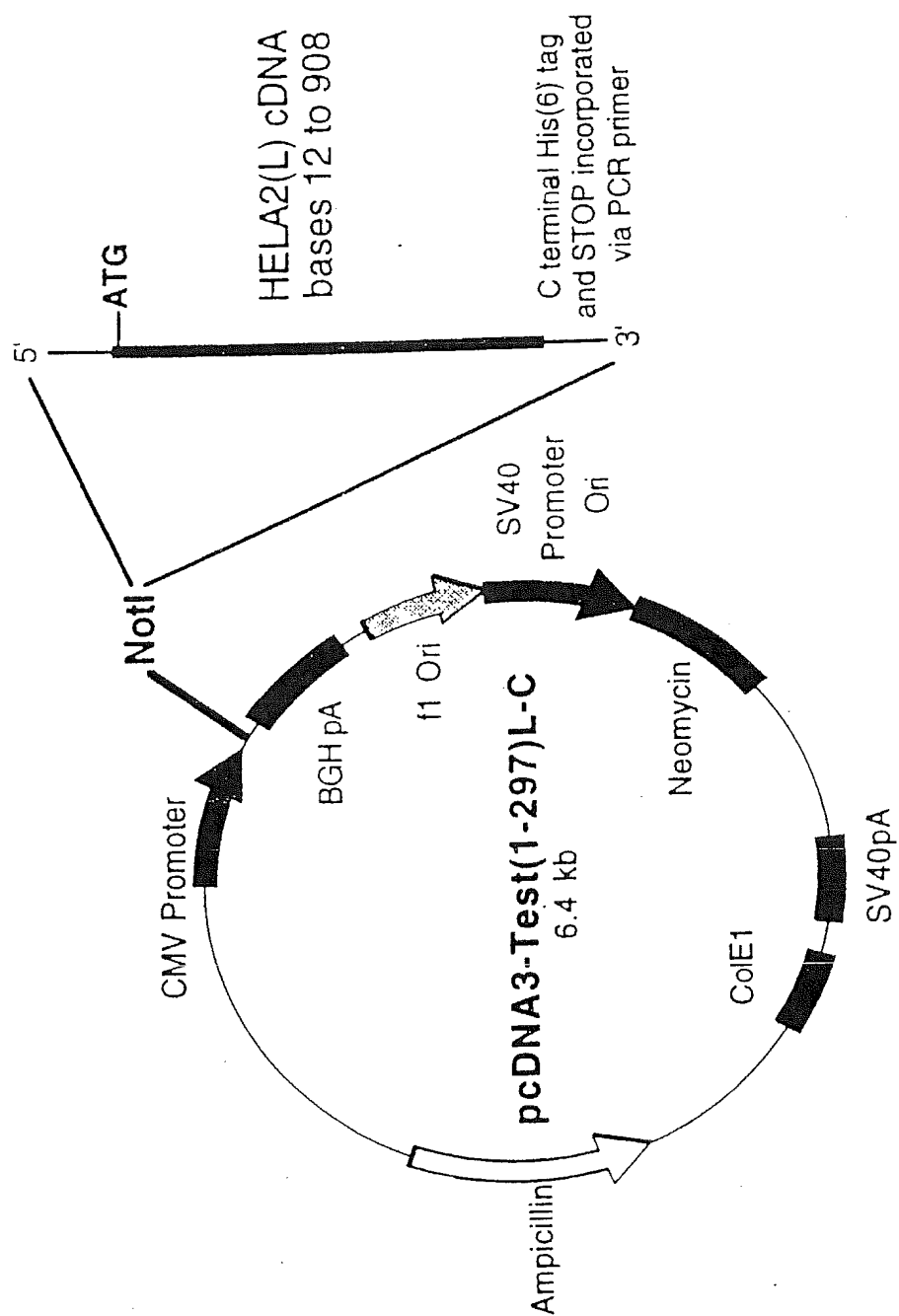


FIG 8(iii)

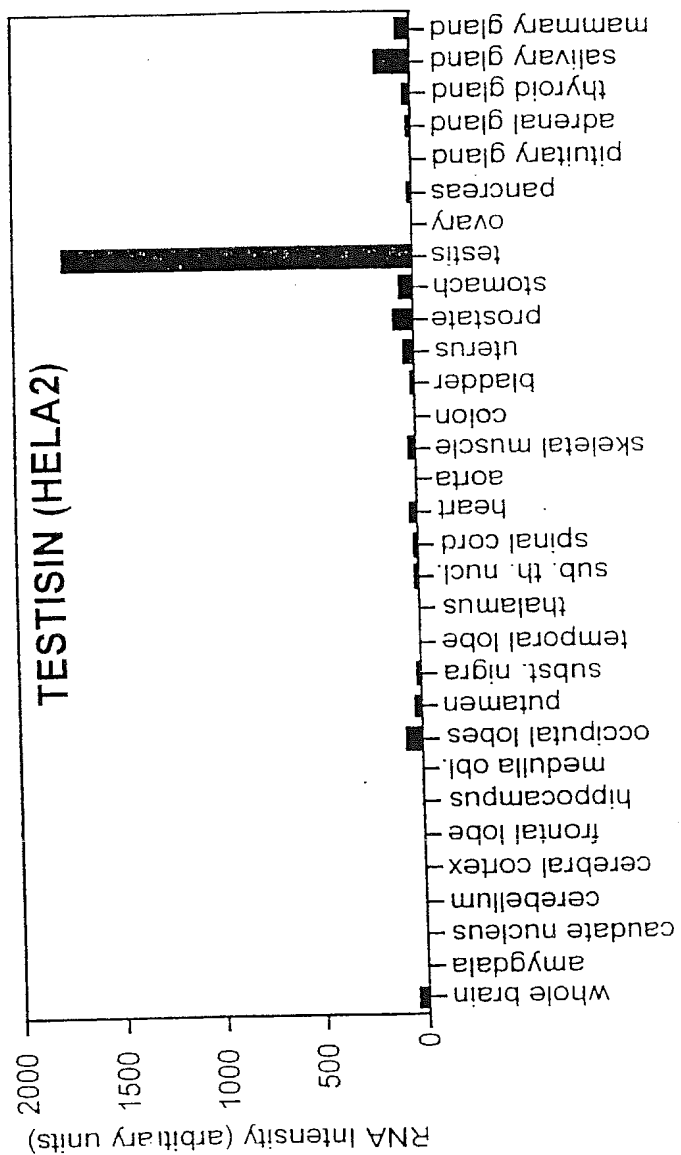
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FIG 9

<u>FIG 9(i)</u>	<u>FIG 9(ii)</u>
<u>FIG 9(iii)</u>	<u>FIG 9(iv)</u>

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FIG 9(i)



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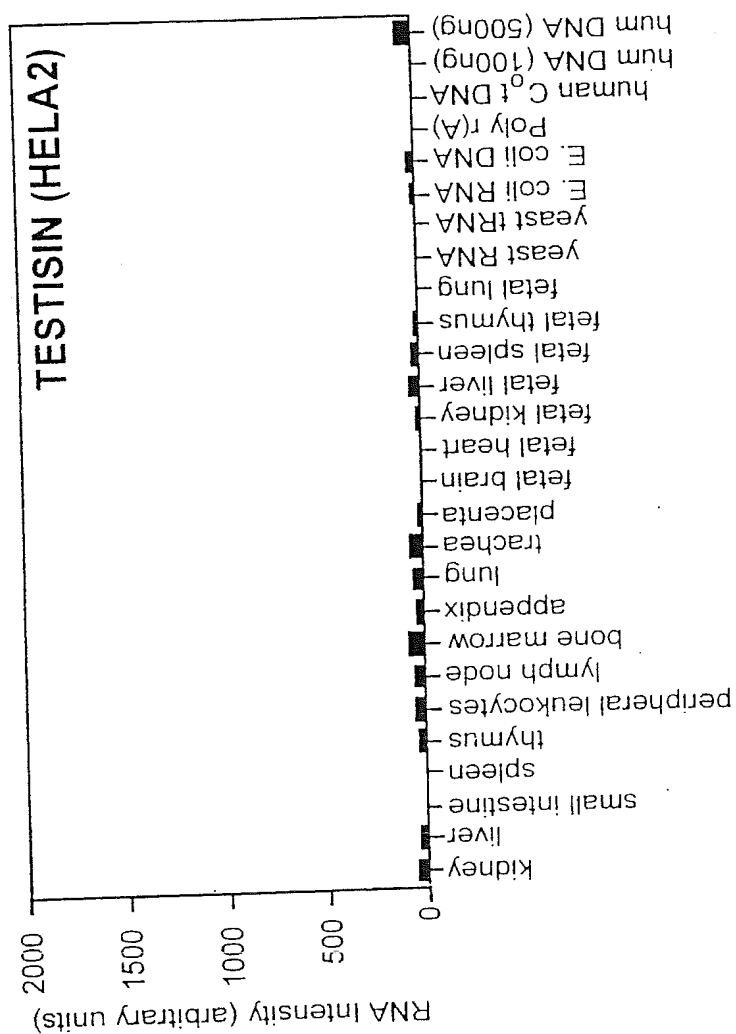
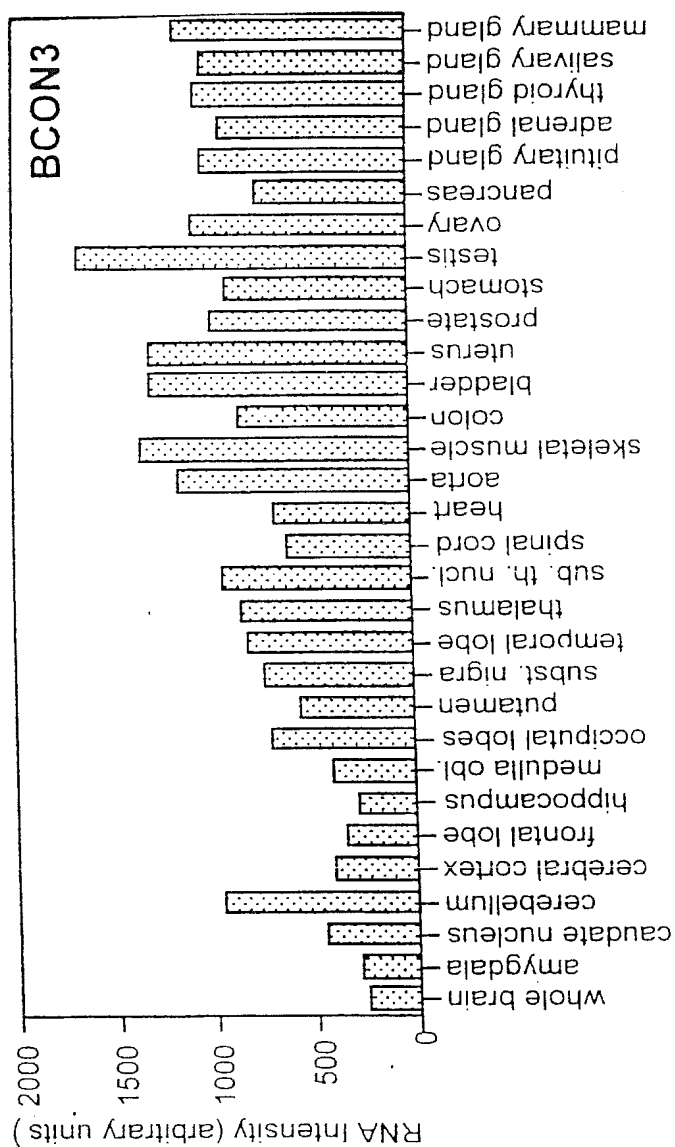


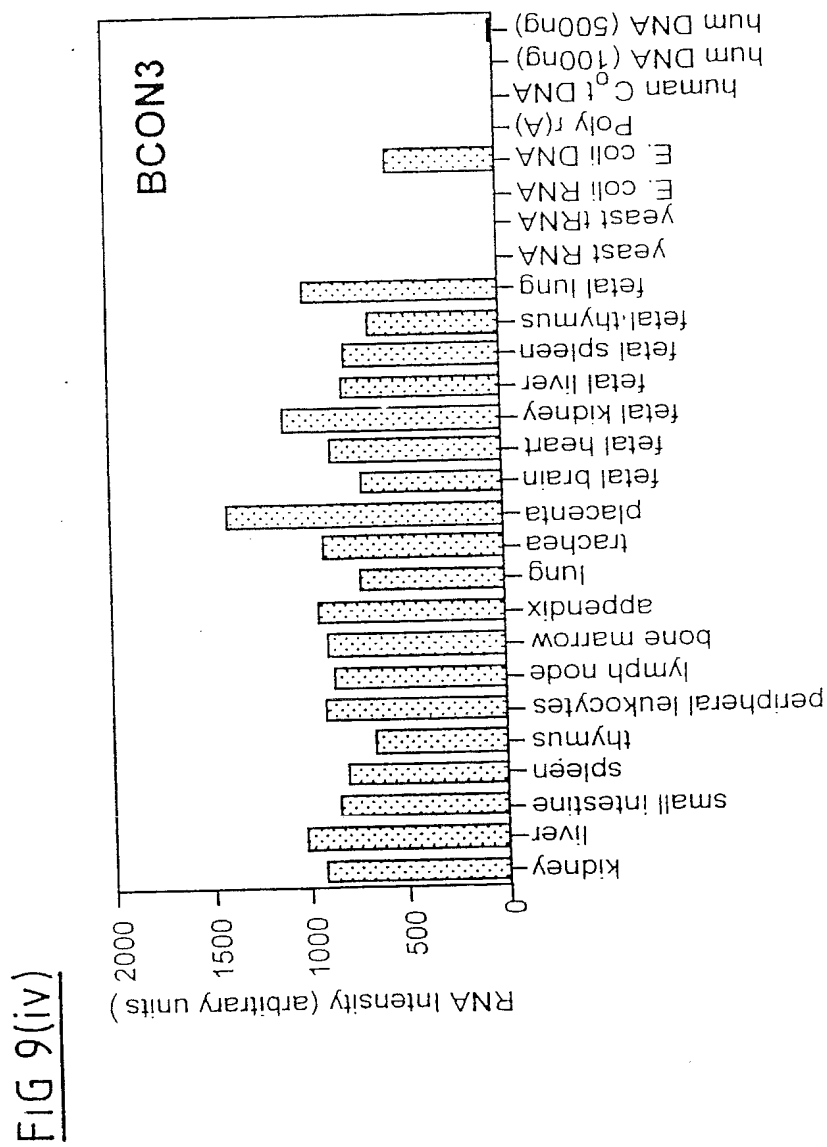
FIG 9(ii)

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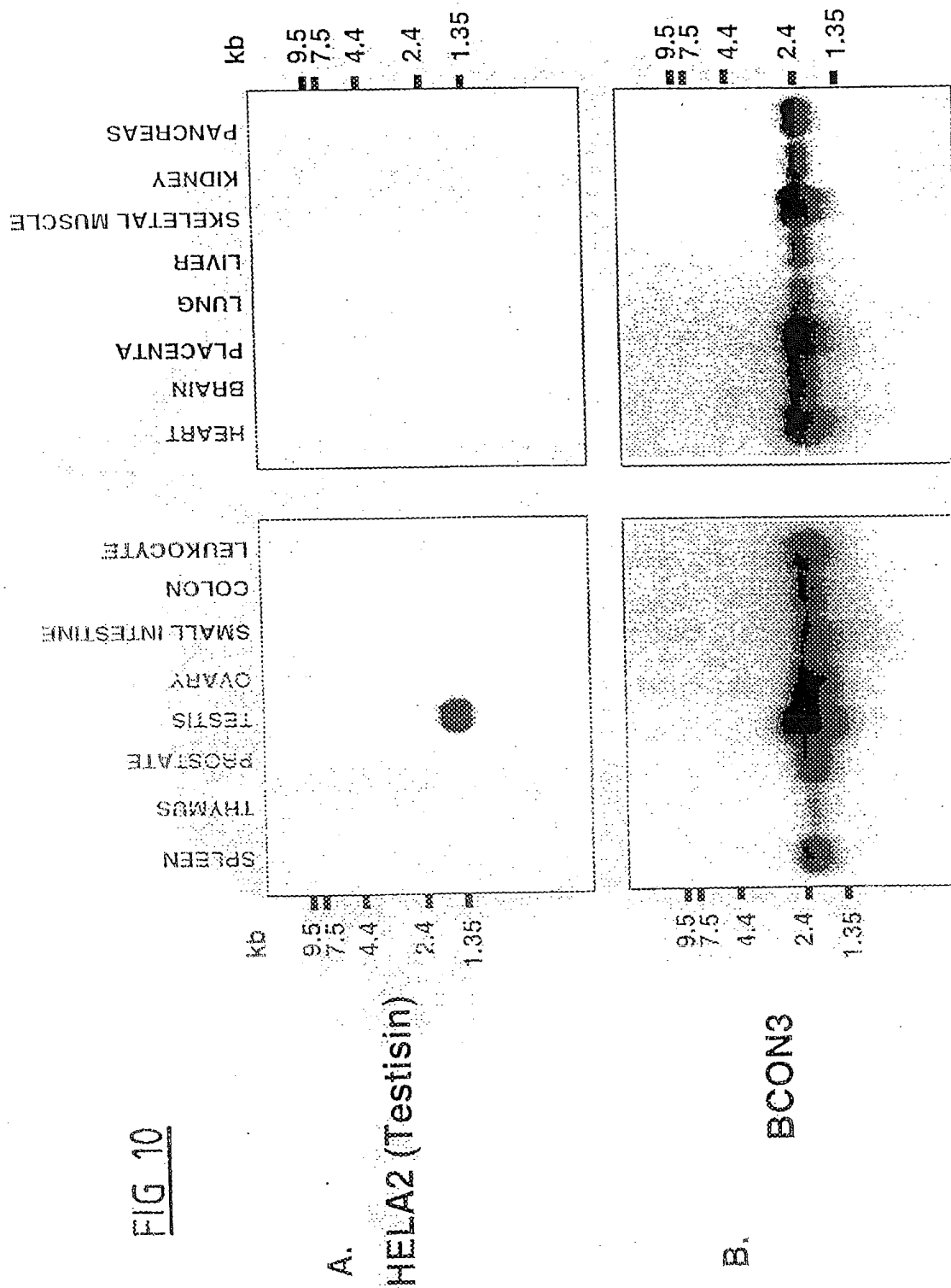
FIG 9(iii)



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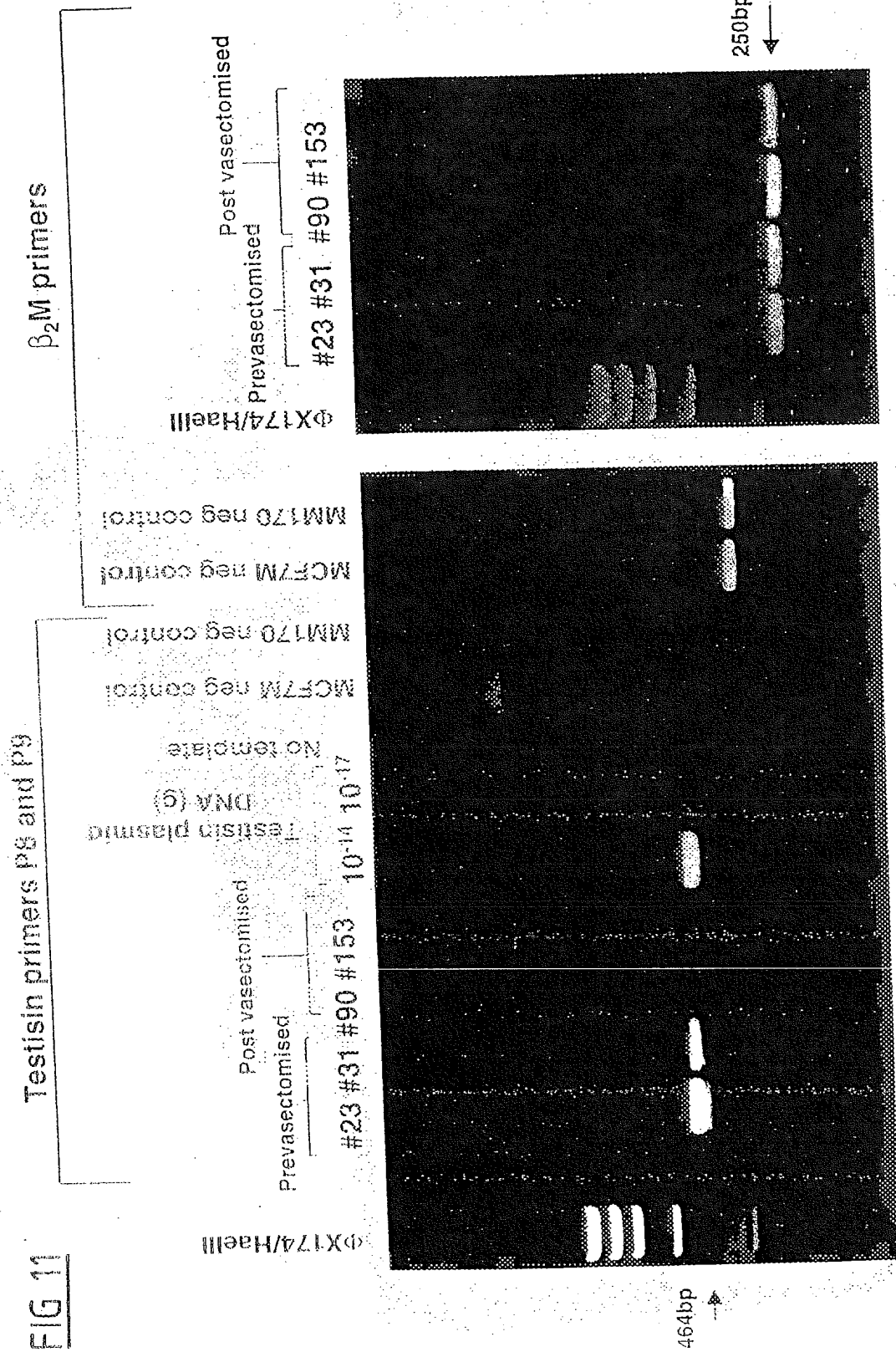


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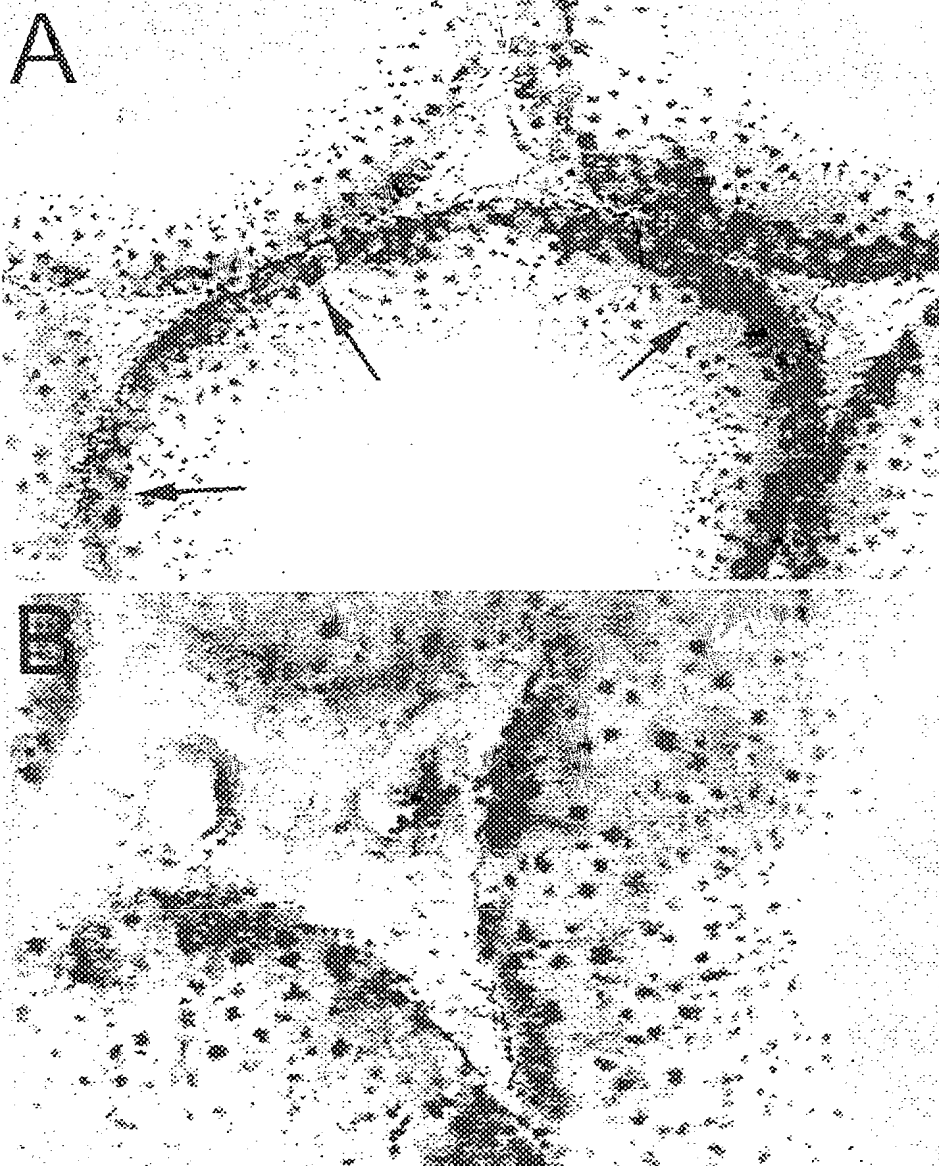


FIG 12

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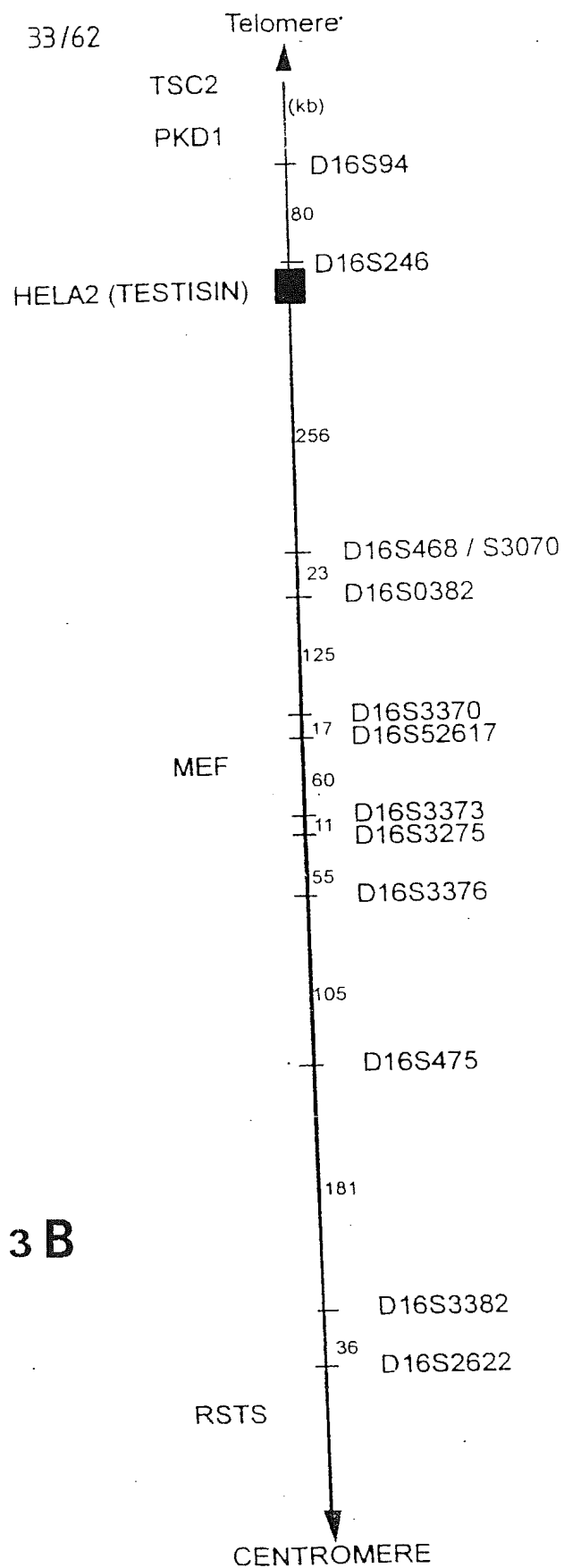
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Testis (HELA2) is located on human chromosome 16p13.3



FIG 13A

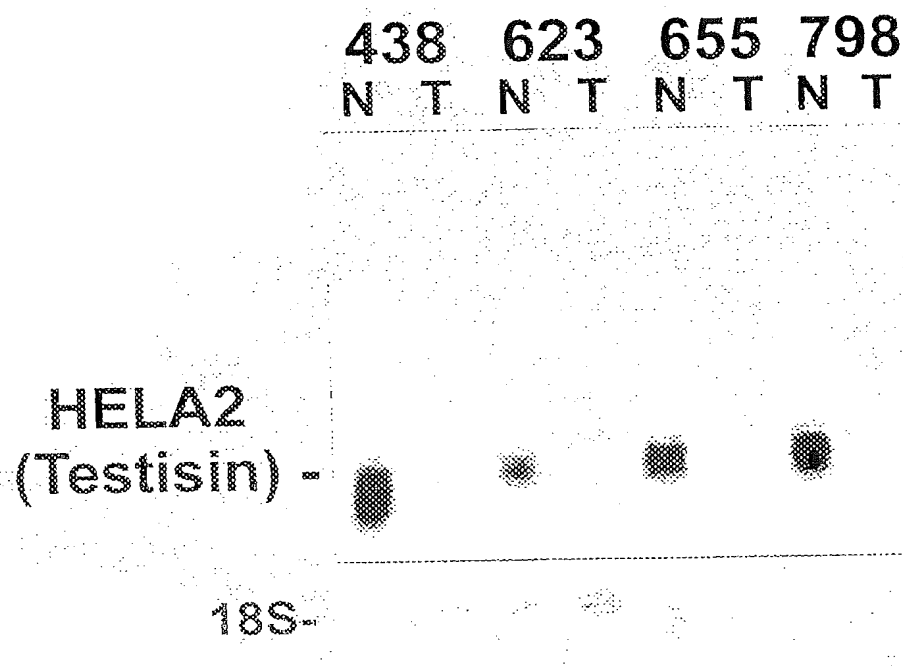
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**FIGURE 13 B**

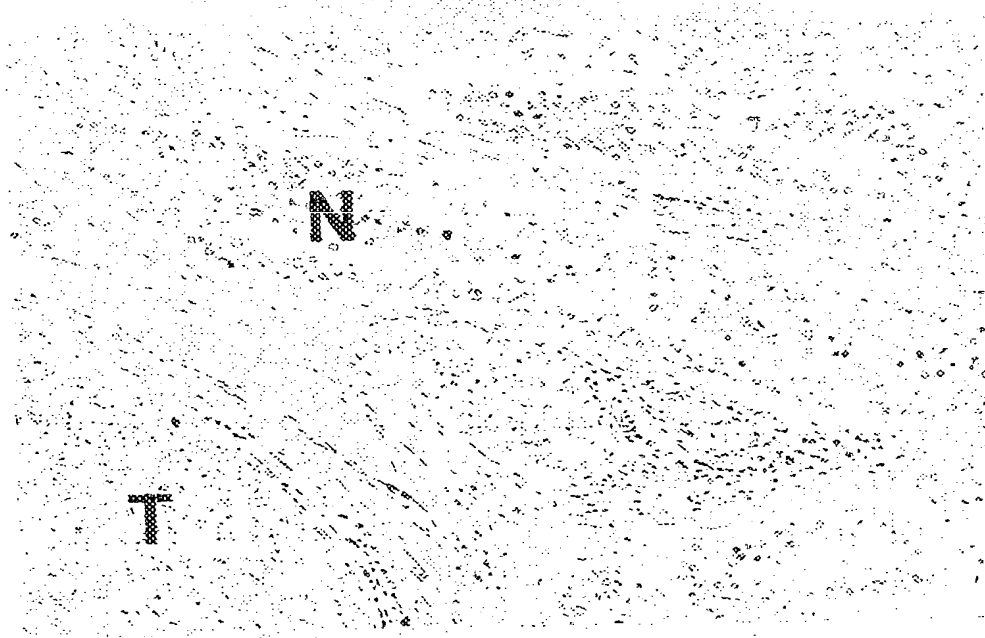
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FIG 14 34/62

A. Northern Blot



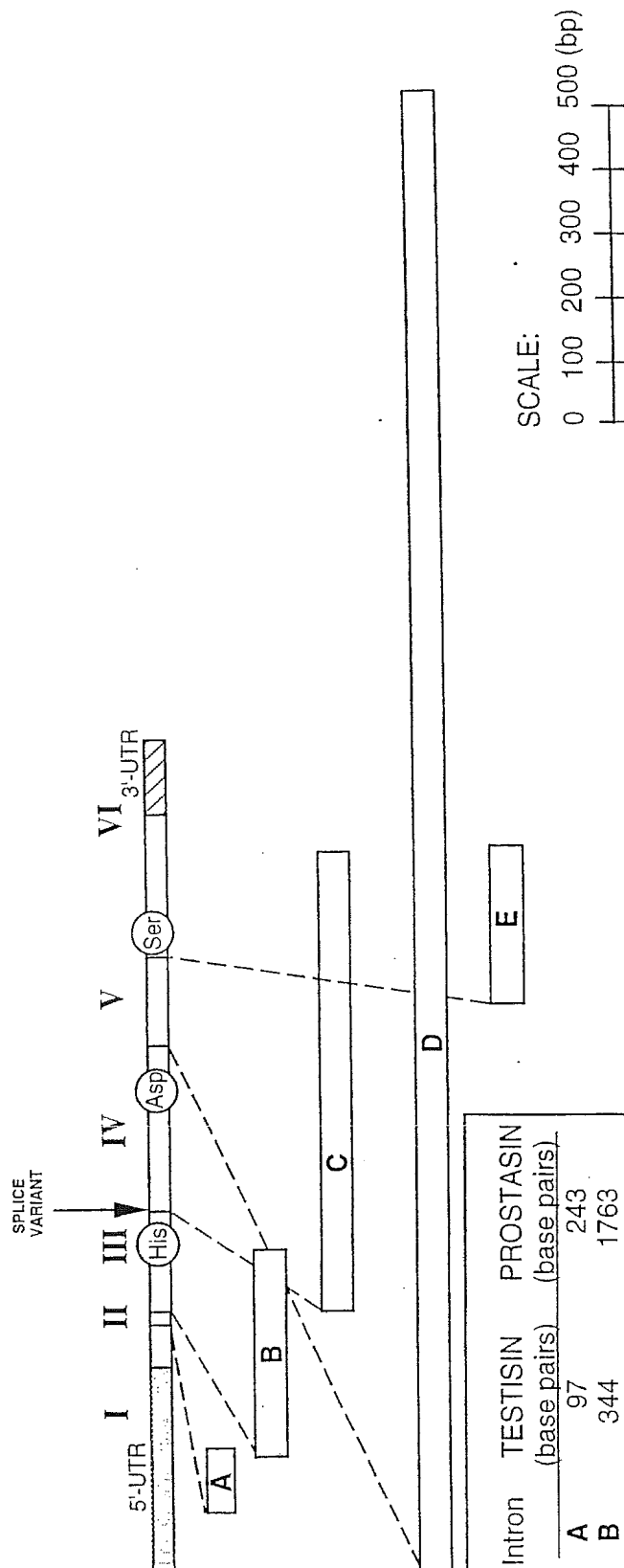
B. Immunohistochemistry



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TESTISIN INTRON/EXON BOUNDARIES AND SIZES



SCALE:

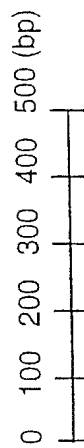


FIGURE 15

Intron	TESTISIN (base pairs)	PROSTASIN (base pairs)
A	97	243
B	344	1763
C	716	271
D	~2200	85
E	256	92

Exon	TESTISIN (base pairs)	PROSTASIN (base pairs)
I	>76	417
II	18	18
III	163	163
IV	284	272
V	168	167
VI	348	899

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FIG 16

<u>FIG 16(i)</u>
<u>FIG 16(ii)</u>
<u>FIG 16(iii)</u>
<u>FIG 16(iv)</u>
<u>FIG 16(v)</u>
<u>FIG 16(vi)</u>

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```

50  agtgagtctc ctgcctcagc ctcccaagta gctgggactt cagggtgtgtg
100 ccaccatcct cagctaattt tttttttttt tttttttttg agaaggagtc
150 ttgctctgtc gcccaggctg gagtgcagtg gcgcgatctt ccaggcccca
200 ccgggccctc aggaaggcct tgccctacctg ctttaagggg actcctggct
250 cagggccagg cccctggtgc tggaggaggt ggtgggtgga gggcaggggg
300 caccaagcgg gcagccagga cccccgggt gcagacaaga aaaggactgt
      /+1...EXON 1...
350 ggggtccacc ggtctgtggc cACATCAAGG AATGTGGTTG AAGACCCGCC
400 CTTAGGAGCT GAAAGCCAGG GCGCTACCAG GCCTGAGAGG CCCCAACAG
450 CCTTGGGCC TGGTTTGGGA GGATTAACT GGAGCTCCCA ACCCGCCCTG
500 CCCCCAGGG GCGACCCCGG GCCCGGCGG AGAGGAGGCA GAGGGGCGT
550 CAGGCCGCGG GAGAGGAGG CATGGGCGG CGCGGGCGG TGCTGCTGGC
      /INTRON A...
600 GCTGCTGCTG GCTCGGGCTG GACTCAGGAA GCCGGgtgag ctcggggcgc
650 tgctggcggg atggggaggc gggggagcgg tggggaggac gggagggtgga

```

FIG 16(i)

700	g gccgcgggg agtcacttct tgtctccgc agAGTCGCAG GAGGCGGCGC	/EXON 2...
750	CGTTATCAGg tagggcgccc aggacgcgcg attcctgcca gggccgttgg	/INTRON B...
800	gccgaggtgg acggggggcg gtgagggggt agaggggggc ctttactgct	
850	ctctcgcccc cgcccccggg atcgagaaact ctgttggcgt ggaaagtaac	
900	taacggacgc tggaggggga tgggcgggcc ctgcagagca cgtgggagga	
950	tctccagtgt cacctacttc ctgctgcaca cacgcgaggg gacctgggt	
1000	gggcaaaaac gtgctttccc ggacgggggt gaaggggaga aagggagagg	
1050	tcgggcttgg ggggctgcct cccgcggctc agcagttcct ctgaccatcc	
1100	gagGACCATG CGGCCGACGG GTCATCACGT CGCGCATCGT GGGTGGAGAG	/EXON 3...
1150	GACGCCGAAC TCGGGCGTTG GCCGTGGCAG GGGAGCCTGC GCCTGTGGGA	
1200	TTCCCAACGTA TCGGGAGTGA GCCTGCTCAG CCACCGCTGG GCACTCACGG	

FIG 16(ii)

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/INTRON C...
CGGCGCACTG CTTTGAAACg tgagtggggg tgcgaacgga ggggtgcggg 1250
gacgggcagg aacagggctg gagggagtgc caccgaactt tacctctggt 1300
ctgatgccag acttgggcgt gaaagtgtg cgtggatgcg gcctgggtgtt 1350
ctcctgagcc ccaggctgtg ctgcagccgg ttacaccac tccagttccc 1400
tttgggtctc ctggaggga ccctgttcag gttattccag aatgttcttc 1450
cagaacattt ccacacatt ttgggtattc tctccctttt tctttcaacc 1500
caaagttcac cactgaccat cccaccctca tccccctcc tggtaggacgg 1550
tgcggtacag tgtggggcac tgagccaaagg ccagcaccac cgggccgctg 1600
tgtggactcc atcctgccaa tcccacattg gcgtgggtgca tctccccatt 1650
cctccttggg ctgcatgggg gtgccccctgg aggccttggc tcaatgcaag 1700
gctccttggg acagctctgg gaggtgacaa gacccaccc ttctgctgca 1750
ggagcaggtc ctaggacttt ggttgtggtc tgtctgggct ccttcatttc 1800
tgcaggggac cctgggtgtt agcaagtagc agcaacacca cagtttcccc 1850
tcctgcactg gacccagtt gtgctcaggt agccagccct ccatccaggg 1900

FIG 16(iii)

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/EXON 4...

1950 cccctgactg ctctcttctc ttctgccagc tatagTGACC TTAGTGATCC
 2000 CTCCGGGTGG ATGGTCCAGT TTGGCCAGCT GACTTCCAAG CCATCCTTCT
 2050 GGAGCCTGCA GGCCTACTAC ACCCGTTACT TCGTATCGAA TATCTATCTG
 2100 AGCCCTCGCT ACCTGGGGAA TTCACCCCTAT GACATTGCCT TGGTGAAGCT
 2150 GTCTGCACCT GTCACCTACA CTAACACAT CCAGCCCATC TGCTCTCCAGG
 2200 CCTCCACATT TGAGTTTGAG AACCGGACAG ACTGCTGGGT GACTGGCTGG

/INTRON D...

2250 GGGTACATCA AAGAGGATGA GGgtgaggct ggggacaggc ggggtcagggg
 2300 ggaactgtct ttgttcacct gtccccctgc ataggcacia tagccccctg
 2350 cttggtcttg ggggtgcaggc tatgccccctc ttgcttgagc tctctcctca
 2400 cctgccaggg cagggaccaa acacccagtt ctctcccttc caggggctgt
 2450 gggggccaga aggagagtgt gagaggagg ccagtttggc gcaagcctgt
 2500 ggggtggtgc gtggtggagg ggcttctggag ggcttggcga cataaacctc
 2550 atacttggat ttattcctgc atctttccac ctccccagc gctcaccaat

FIG 16(iv)

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```

gccccaggca tca.....approx 1000 bp.....
ccagggtgcc cttcccccaggcttggct ttggatgctt atgtgaacac
cgttttaagt tgccttgcc ccttcctcgg ttcctttttg gctgaggaat
ctctccatgg ctgcaggcag ggcattgtt gccattctac agatagggaa
agtgcggctg ggggagctct gacagctgtc cctccccggg gccttctgtg
atgtctgctga gggcctctgt tgtgctgggg tctgggttgg agctgggggt
aatggagatg aacctgccag gcacagtggg tgccccaggg cccccacccc
cgcagcctat gccatccctc catagagggg cctcaggttg ctgtctctct
                                /EXON 5...

ccttcccact atcgtccgca cagCACTGCC ATCTCCCCAC ACCCTCCAGG
AAGTTCAGGT CGCCATCATA AACAACTCTA TGTGCAACCA CCTCTTCCTC
AAGTACAGTT TCCGCAAGGA CATCTTTGGA GACATGGTTT GTGCTGGCAA
                                /INTRON E...

TGCCCCAAGGC GGAAGGATG CCTGCTTCgt gagtgcctt gccaccactc
ccagccccagg aaagcctcct gtgtccctgt gccttatttg accctcatgc
caacccccggg aggtggagac tgttgcccc ctctgcagat gcagaaacgg

```

FIG 16(v)

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~4263
 ~4313
 ~4363
 ~4413
 ~4463
 ~4513
 ~4563
 ~4613
 ~4663
 ~4713
 ~4763
 ~4813
 ~4863
 ~4866

aggccttggt gctgccaggg ggaggaggag gatgtgcacc cagtctaccc
 agccccatag cccttccac tctcagcccc tccccgtccc cactcactct
 /EXON 6...
 gccccaggct gacctcagcc ccgctgctcc ccagGGTGAC TCAGGTGGAC
 CCTTGGCCTG TAACAAGAAT GGACTGTGGT ATCAGATTGG AGTCGTGAGC
 TGGGGAGTGG GCTGTGGTCG GCCCAATCGG CCCGGTGTCT ACACCAATAT
 CAGCCACCAC TTTGAGTGGA TCCAGAAGCT GATGGCCCAG AGTGGCATGT
 CCCAGCCAGA CCCCTCCTGG CCGCTACTCT TTTTCCCTCT TCTCTGGGCT
 CTCCCACCTCC TGGGGCCGGT CTGAGCCCTAC CTGAGCCCAT GCAGCCTGGG
 GCCACTGCCA AGTCAGGCCCT TGGTTCTCTT CTGCTCTTGT TGGTAATAAA
 CACATTCCAG TTGATGCCCTT GCAGGGCATT CTTCaaaagc agtgggcttca
 tggacagctc attctctctt gtgcagacag cctgtctgtg cccctggctc
 acacccacat ctgttctgca ccatagaacc atctggttat ttcgatcaga
 aagagaattg tgtgttgccc aggcctgggtc tgaacgccta ggggtgtctcg
 atc

FIG 16(vi)

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EXON III CACTGCTTTGAAAC**gt**gagtgggggtgcgaacggag
 ggggtgcggggacggggcaggaacaggggctggagggagtgccaccga
 actttacctctggtctgatgccagacttgggcgtgaaagttgtgc
 gtggatgcggcctggtgttctcctgagccccaggctgtgctgcag
 cgggttacaccactccagttccctttgggtctcctggaggggaac
 cctgttcagggttattccagaatgttcttccagaacatttccacac
 actttttgggtattctctccctttttcttttcaacccaaagttcacc
 actgaccatcccaccctcatccccctcctggtggacgggtgcggt
 acagtgtggggcactgagccaaggccagcacccccgggcccgtgt

.....INTRON C (716 BP).....

gtggactccatcctgccaatcccacattggcgtggtgcatctccc
 cattcctccttgggctgcatgggggtgcccctggagggccttggct
 caatgcaaggctccttgggacagctctgggaggtgacaagacccc
 acccttctgctgcaggagcaggtcctagactttggttgtggtctg
 tctgggctccttcatttctgcaggggaccctgggtgttagcaagt
 agcagcaacaccacagtttcccctcctgcactggaccccagttgt
 gctcaggtagccagccctccatccagggcccctgactgctctctt
 ctcttctgccc**ag**ctat**ag**TGACCTTAGTGATCCC EXON IV

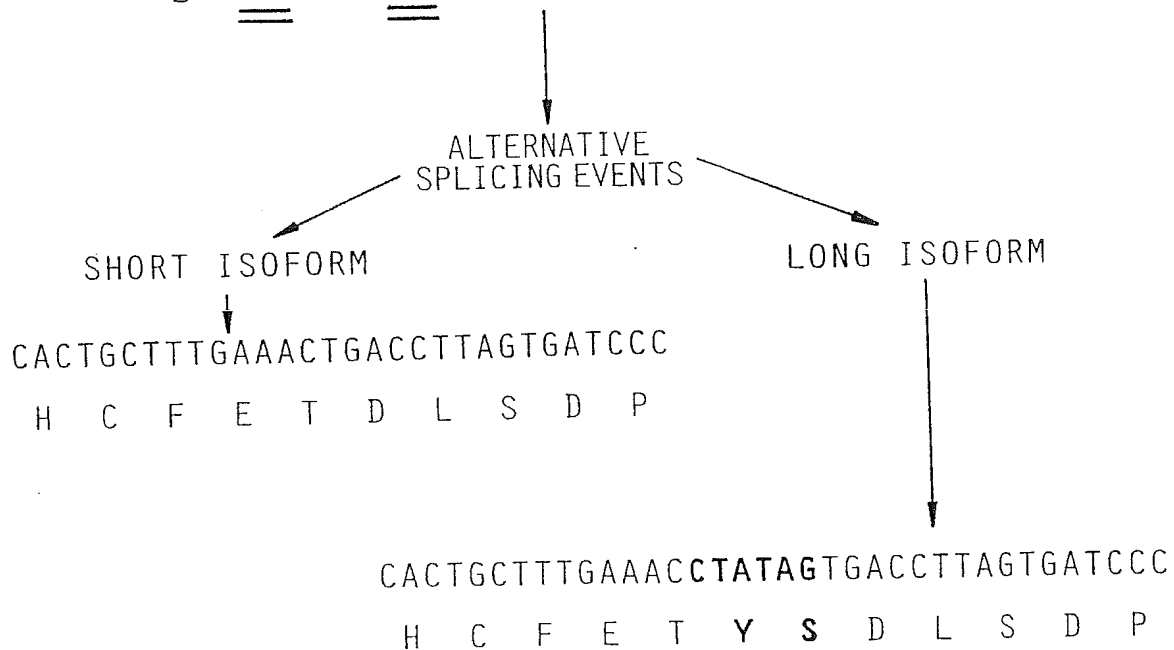


FIGURE 17

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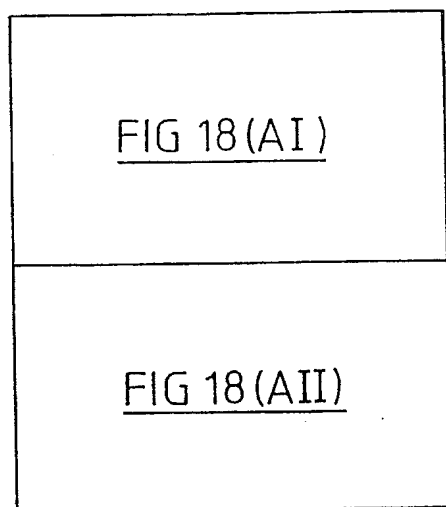


FIG 18(A)

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FIGURE 18 (AI)

1 CGACCTATTGTCAGGGCCCTGCGGTACAGGACCATCCCTTCCCGTATAGTGGTGGCGA 20
D L L S G P C G H R T I P S R I V G G D
61 TGATGCTGAGCTTGGCCCGCTGGCCCGTGGCAAGGAGCCCTGCGTGTATGGGCAACCACCTT 40
D A E L G R W P W Q G S L R V W G N H L
121 ATGTGGCGCAACCTTGTCTCAACCGCCGCTGGGTGCTTACAGCTGCCCACTGCTTCCAAAA 60
C G A T L L N R R W V L T A A H C F Q K
181 GGATAACGATCCCTTTTGACTGGACAGTCCAGTTTGGTGAGCTGACTTCCAGGCCATCTCT 80
D N D P F D W T V Q F G E L T S R P S L
241 CTGGAACCTACAGGCCCTATTCCAACCGTTACCAAATAGAAGATATTTCTGAGCCCCAA 100
W N L Q A Y S N R Y Q I E D I F L S P K
301 GTACTCGGAGCAGTATCCCAATGACATAGCCCTGCTGAAGCTGTCACTCTCCAGTCACCTA 120
Y S E Q Y P N D I A L L K L S S P V T Y
361 CAATAACTTCATCCAGCCCATCTGCCCTCCTGAACCTCCACGTACAAGTTTGAGAAACCGAAC 140
N N F I Q P I C L L N S T Y K F E N R T
421 TGA CTGCTGGGTGACCGGCTGGGGGGCTATTGGAGAAGATGAGAGTCTGCCATCTCCCAA 160
D C W V T G W G A I G E D E S L P S P N

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FIGURE 18 (AII)

481 CACTCTCCAGGAAGTGCAGGTAGCTATTATCAACAACAGCATGTGTAACCATATGTACAA
T L Q E V Q V A I I N N S M C N H M Y K 180

541 AAAGCCAGACTTCCGCACGAAACATCTGGGAGACATGGTTTGGCTGGCACTCCTGAAGG
K P D F R T N I W G D M V C A G T P E G 200

601 TGGCAAGGATGCCTTGTGACTCGGAGGACCCCTTGGCCCTGCGACCAAGGATACGGT
G K D A C F G D S G G P L A C D Q D T V 220

661 GTGGTATCAGGTTGGAGTTGTGAGCTGGGGAATAGGCTGTGTCGCCCAATCGCCCTGG
W Y Q V G V S W G I G C G R P N R P G 240

721 AGTCTATACCAACATCAGTCATCACTACTAACAAGTCCAGTCAACCATGATCCGCAATGG
V Y T N I S H H Y N W I Q S T M I R N G 260

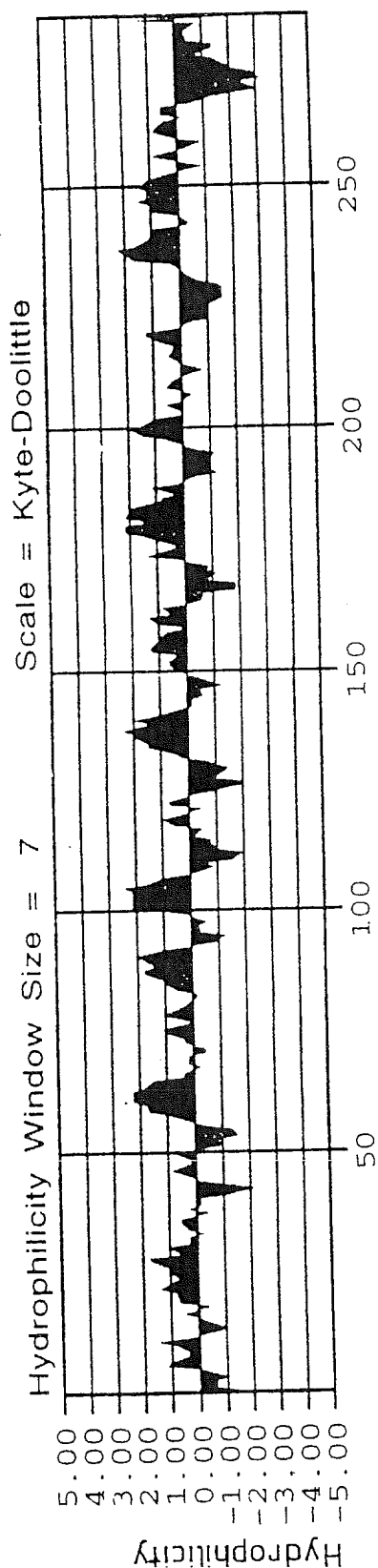
781 GCTGCTCAGCCCTGACCCAGTCCCCTTGCTACTGTTTCTTACTCTGGCCCTGGGCTTCCTC
L L R P D P V P L L L F L T L A W A S S 280

841 TTTGCTGAGGCCCTGCCCTGAGCCCAACACGTGTACGTCACACCTGTGAGGTCAGGGTGTGTC
L L R P A 285

901 TCCTTTGTATCTTGCTTGCTAATAAACCTGTTAATATTAAAAAATAAAAAA

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FIG 18B



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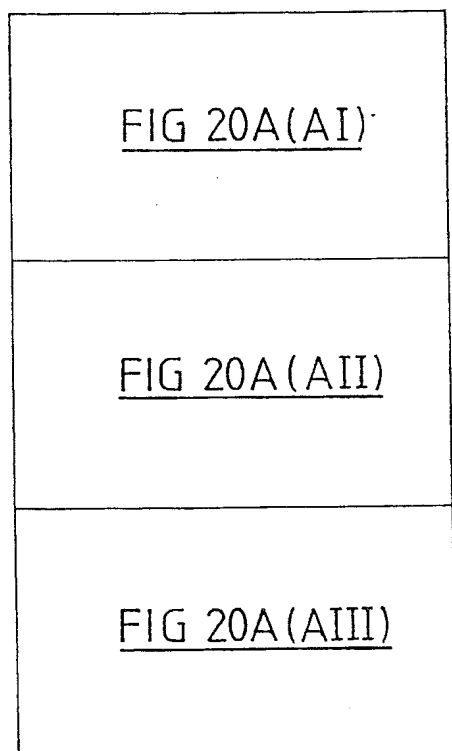


FIG 20A(A)

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FIGURE 20A (AI)

CTGAACCGGTTGTGGCGCGGAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGAGC 60
1 L N R ∇ V V G G E D S T D S E W P W I V S
ATCCAGAAGAAATGGGACCCACCACTGCGCAGGTTCTCTGCTCACCAGCCGCTGGGTGATC 120
21 I Q K N G T H H \square A G S L L T S R W V I
ACTGCTGCCCACTGTTTCAAGGACAAACCTGAACAAACCATACCTGTTCTCTGTGCTGCTG 180
41 T A A \textcircled{H} \square F K D N L N K P Y L F S V L L
GGGCGCTGGCAGCTGGGGAACCCCTGGCTCTCGGTCCAGAAAGTGGGTGTTGCCCTGGGTG 240
61 G A W Q L G N P G S R S Q K V G V A W V
GAGCCCCACCCCTGTGTATTCTGGAAGGAAGGTGCCCTGTGCAGACATTGCCCTGGTGCGT 300
81 E P H P V Y S W K E G A C A \textcircled{D} I A L V R
CTCGAGCGCTCCATACAGTTCTCAGAGCGGGTCCCTGCCCATCTGCCCTACCTGATGCCCTCT 360
101 L E R S I Q F S E R V L P I \square L P D A S
ATCCACCTCCCTCCAAACACCCCACTGCTGGATCTCAGGCTGGGGGAGCATCCAAGATGGA 420
121 I H L P P N T H \square W I S G W G S I Q D G

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FIGURE 20A (AII)

GTTCCCTTGCCCCACCCCTCAGACCCCTGCAGAAGCTGAAGTTCTCTATCATCGACTCGGAA 480
 141 V P L P H P Q T L Q K L K V P I I D S E

 GTCTGCAGCCATCTGTACTGGGGGAGCAGACAGGACCCATCACTAGGACATGCTG 540
 161 V [C] S H L Y W R G A G Q G P I T E D M L

 TGTGCCGGCTAACTTGGAGGGGAGCGGGATGCTTGTCTGGCGACTCCGGGGGCCCCCTC 600
 181 [C] A G Y L E G E R D A [C] L G D [S] G G P L

 ATGTGCCAGGTGGACGGCGCCTGGCTGCTGGCCGGCATCATCAGCTGGGGCGAGGCTGT 660
 201 M [C] Q V D G A W L L A G I I S W G E G [C]

 GCCGAGCGCAACAGCCCGGGTCTACATCAGCCCTCTCTGCGCACCGCTCCTGGGTGGAG 720
 221 A E R N R P G V Y I S L S A [H] R S W V E

 AAGATCGTGCAAGGGGTGCAGCTCCGCGGGCGGCTCAGGGGGGTGGGGCCCTCAGGGCA 780
 241 K I V Q G V Q L R G R A Q G G A L R A

 CCGAGCCAGGCTCTGGGGCCGCGGCTCCTAGGGCCCAAGCGGACGCGGGGCTCGG 840
 261 P S Q G S G A A R S

 ATCTGAAAGCGGCAGATCCACATCTGGATCTGGATCTGCGCGCGCCCTCGGGCGGTTTC 900
 CCGCGCGTAAATAGGCTCATCTACCTCTACCTCTGGGGGCGCGGACGGCTGCTCGGAA 960

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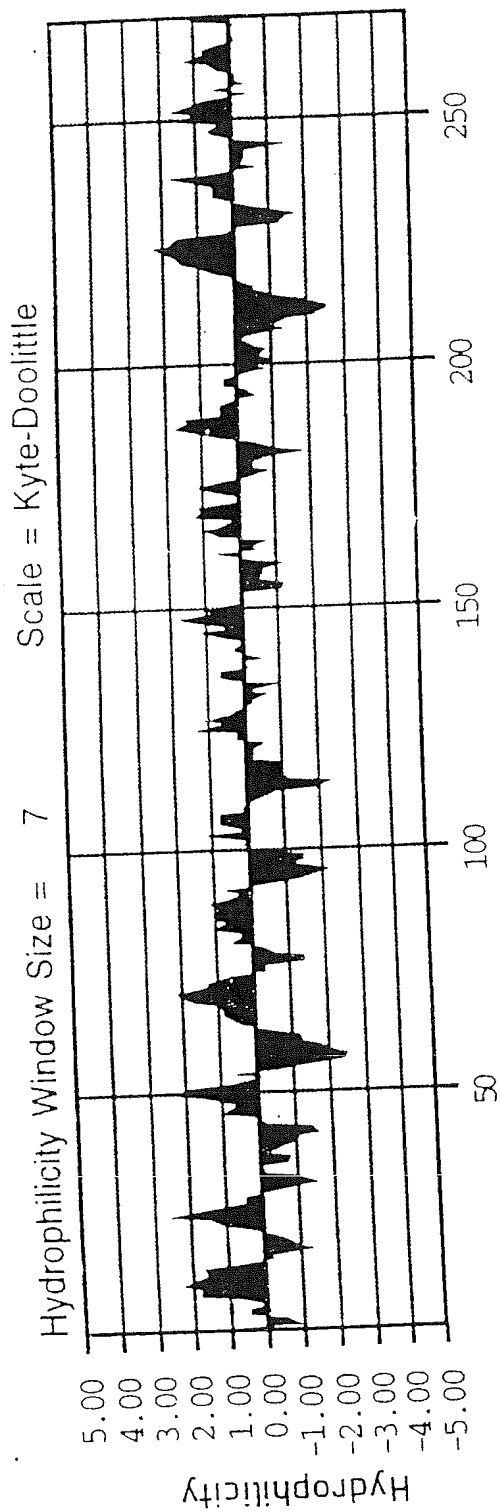
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FIGURE 20A (AIII)

AGGAAACCCCTCCCGACCCGACGGCCCTCAGGCCCGCCCTCCAAGGCATCAGGCC 1020
CCGCCCAACGGCCCTCATGTCCCGCCCCACGACTTCCGGCCCCCGGGCCCCCAGCG 1080
CTTTGTGTATATAAATGTTAATGATTTTATAGGTATTGTAAACCCCTGCCACATATCT 1140
TATTATTCCCTCCAATTCAATAA

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FIG 20A (B)



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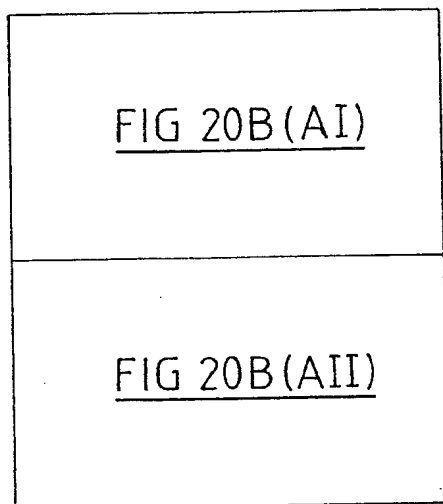


FIG 20B(A)

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FIGURE 20B (AI)

1 AATGCGGCCACTCCAAGGAGCGCGGAGGATTGTGGAGGCCAAGACACCCAGGAAGAC 60
 [C] G H S K E A G R V I V G G Q D T Q E G
 21 R W P W Q V G L W L T S V G H V [C] G G S
 GCTGGCCGTGCGAGGTTGGCCTGTGGTTGACCTCAGTGGGGCATGTATGTGGGGGCTCCC 120
 41 L I H P R W V L T A A (H) [C] F L R S E D P
 TCATCCACCCACGCTGGGTGCTCACAGCCGCCCACTGCTTCTGAGGTCTGAGGATCCCG 180
 61 G L Y H V K V G G L T P S L S E P H S A
 GGCTCTACCATGTTAAAGTCGGAGGGCTGACACCCCTCACTTTCAGAGCCCCACTCGGCCT 240
 81 L V A V R R L L V H S S Y H G T T T S G
 TGGTGGCTGTGAGGAGGCTCCTGTCCACTCCTCATACCATGGGACCCACCAGCGGGG 300
 101 (D) I A L M E L D S P L Q A S Q F S P I [C]
 ACATTGCCCTGATGGAGCTGGACTCCCCCTTGCAGGCCCTCCAGTCCAGCCCATCTGCC 360
 121 L P G P Q T P L A I G T V [C] W V N G L G
 TCCCAGGACCCAGACCCCCCTCGCCATTTGGACCGTGTGCTGGGTAAACGGGCTGGGG 420
 141 V H S G E A L A S V L Q E V A V P L L D
 TCCACTCAGGAGAGGCCCTGGCGAGTGTCTTTCAGGAGGTGGCTGTGCCCCCTCCTGGACT 480

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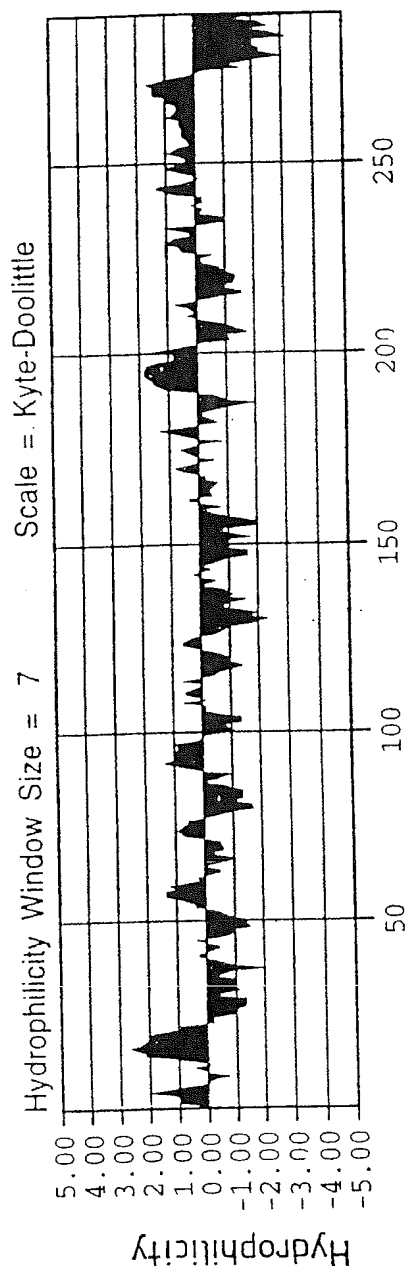
FIGURE 20B (All)

CGAACATGTGTGAGCTGATGTACCACTAGGAGAGCCAGCCTGGCTGGCCAGCGCCTCA 540
161 S N M [C] E L M Y H L G E P S L A G Q R L
TCCAGGACGACATGCTCTGTGCTGGCTCTGTCCAGGGCAAGAAAGACTCCTGCCAGGGTG 600
181 I Q D D M L [C] A G S V Q G K K D S [C] Q G
ACTCCGGGGGGCGCTGGTCTGCCCCCATCAATGATACGTGGATCCAGGCCGGCATTTGTGA 660
201 D [S] G G P L V [C] P I N D T W I Q A G I V
GCTGGGGATTTCGGCTGTGCCCCGGCCTTCCGGCCTGGTGTCTACACCCAGGTGCTAAGCT 720
221 S W G F G [C] A R P F R P G V Y T Q V L S
ACACAGACTGGATTTCAGAGAACCCCTGGCTGAATCTCACTCAGGCATGTCTGGGGCCGCC 780
241 Y T D W I Q R T L A E S H S G M S G A R
CAGGTGCCCCCAGGATCCCACCTCAGGCACCTCCAGATCCCACCCAGTGTGCTGCTTGAGC 840
261 P G A P G S H S G T S R S H P V L L L E
TGTGACCGTATGCTTGTGCTGGTCCCTGTGAACCATGAGCCATGGAGTCCGGGATCCCC 900
281 L L T V C L L G S L
TTTCTGGTAGGATTGATGGAATCTAATAATAAA

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FIG 20B(B)



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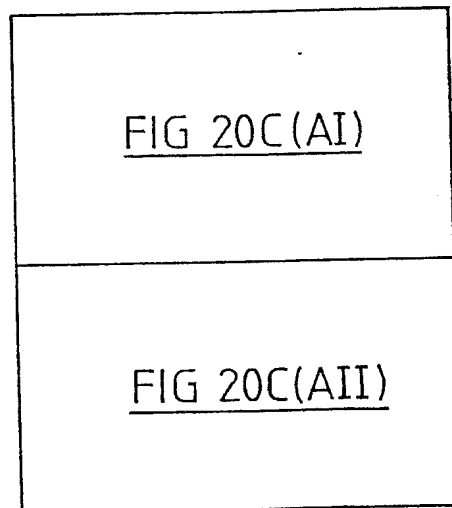


FIG 20C(A)

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FIGURE 20C (AI)

1 CCTGTGTCGCCCCAGGATGCTGAACCGAATGGTGGGGCAGGACACGCAGAGGGCG 60
[C] G R P R M L N R V M V G G Q D T Q E G

21 AGTGGCCCTGGCAAGTCAGCATCCAGCGCAACGGAAGCCACTTCTGCGGGCAGCCTCA 120
E W P W Q V S I Q R N G S H F [C] G G S L

41 TCGCGGAGCAGTGGGTCCTGACGGCTGCGCAGTCTCCGCAACACCTCTGAGACGTCCC 180
I A E Q W V L T A A (H) [C] F R N T S E T S

61 TGTACCAGTCCCTGCTGGGGCAAGGCAGCTAGTGCAGCCGGGACCAACACGCTATGTATG 240
L Y Q V L L G A R Q L V Q P G P H A M Y

81 CCCGGTGAGGCAGGTGGAGAGCAACCCCTGTACCAGGCAGGCCCTCCAGCGCTGACG 300
A R V R Q V E S N P L Y Q G T A S S A (D)

101 TGGCCCTGGTGGAGCTGGAGGCACCAGTGCCCTTACCCAATTACATCCTCCCCGTGTGCC 360
V A L V E L E A P V P F T N Y I L P V [C]

121 TGCCTGACCCCTCGGTGATCTTTGAGACGGGCATGAAGTGGTCACTGGCTGGGGCA 420
L P D P S V I F E T G M N [C] W V T G W G

141 GCCCAGTGAGGAAGACCTCCTGCCCCGAACCGGGATCCTGCAGAACTCGTGTGCCCA 480
S P S E E D L L P E P R I L Q K L A V P

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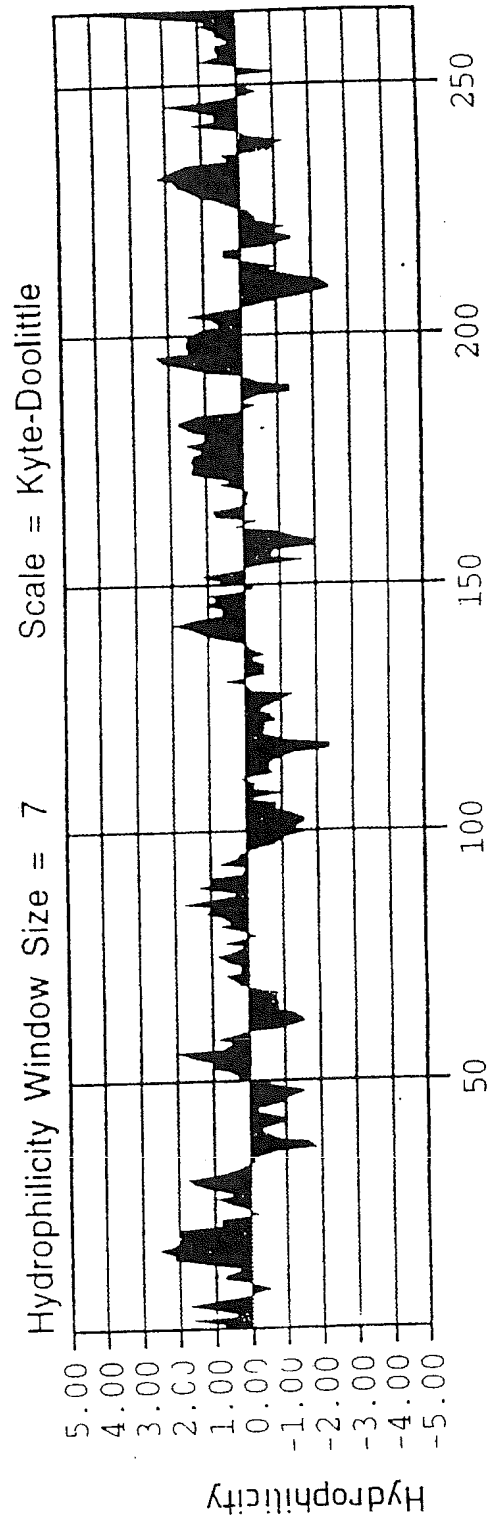
FIGURE 20C (AII)

TCATCGACACACCCAAAGTGCAACCTGCTCTACAGCAAAAGACACCCGAGTTTGGCTACCAAC 540
161 I I D T P K [C] N L L Y S K D T E F G Y Q
CCAAAACCATCAAGAATGACATGCTGTGCGCCGGCTTCGAGGAGGGCAAGAGATGCCT 600
181 P K T I K N D M L [C] A G F E G K K D A
GCAAGGCGACTCGGGCGGCCCCCTGGTGTGCTCGTGGTCAAGTCGTGGCTGCAGGCGG 660
201 [C] K G D (S) G G P L V [C] L V G Q S W L Q A
GGTGATCAGCTGGGGTGAGGGCTGTGCCCGCCAGAACCGCCCGAGGTGTCTACATCCGTG 720
221 G V I S W G E G [C] A R Q N R P G V Y I R
TCACCGCCACCAACTGATCCATCGGATCATCCCCAAACTGCAGTCCAGCCAGCGA 780
241 V T A H H N W I H R I I P K L Q F Q P A
GGTTGGGCGCCAGAAAGTGAGACCCCCCGGGCCAGGAGCCCCCTTGAGCAGAGCTCTGCAC 840
261 R L G G Q K * D P R G Q E P L E Q S S A
CCAGCCTGCCCGCCACACCATCCTGCTGGTCCCTCCAGCGCTGCTGTTGCACCTGTGAG 900
281 P S L P A H T I L L V L P A L L L H L
CCCCACGAGACTCATTTGTAAATAGCGCTCCTCCTCCCTCTCAATAACCTTATTTTA 960
TTTATGTTTCTCCCAATAAA

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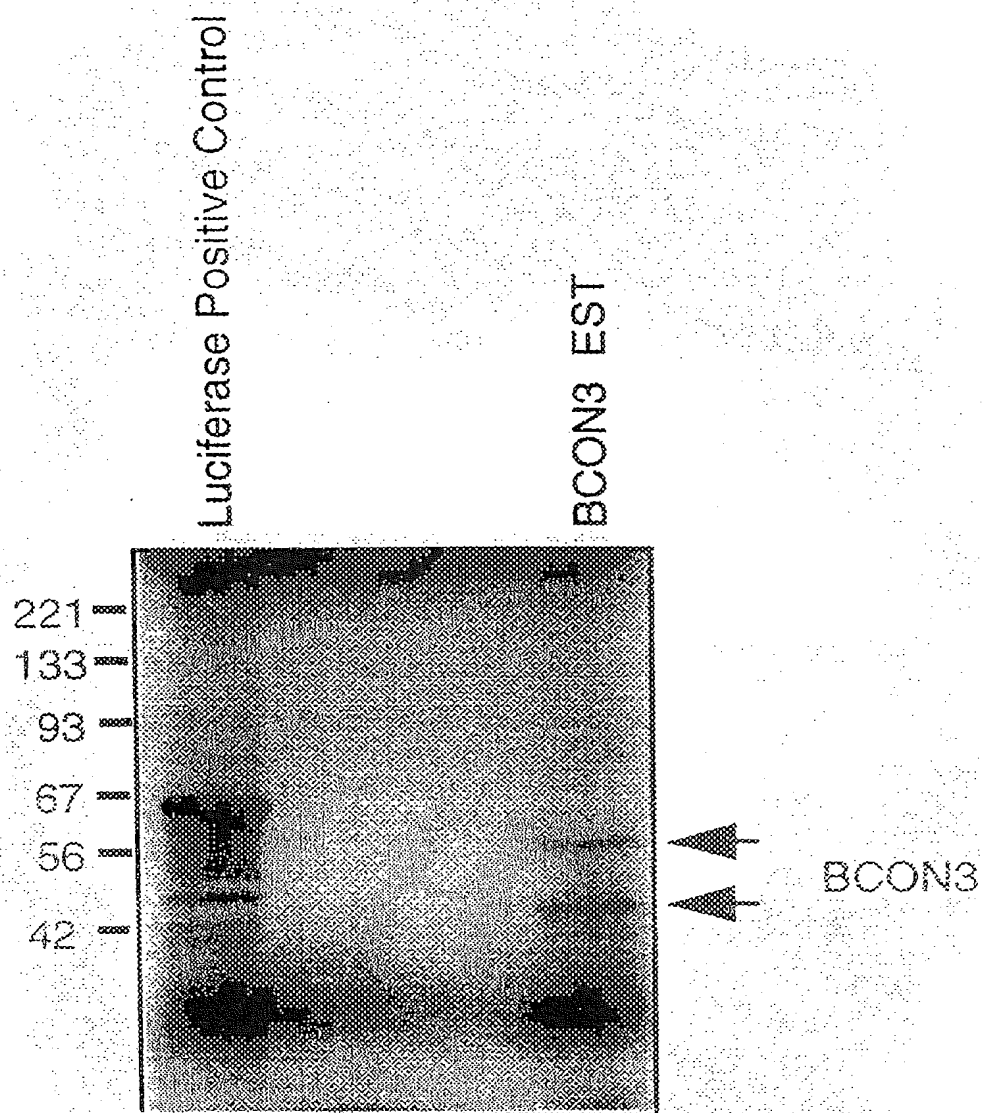
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FIG 20C(B)



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FIG 21

INTERNATIONAL SEARCH REPORT

 International Application No.
 PCT/AU 98/00085

A. CLASSIFICATION OF SUBJECT MATTER		
Int Cl ⁶ : C12N 009/12, 009/64, 015/54, 015/57; C07K 016/40; A61K 038/45, 038/48; C12Q 001/68		
According to International Patent Classification (IPC) or to both national classification and IPC		
B. FIELDS SEARCHED		
Minimum documentation searched (classification system followed by classification symbols) STN (DGENE) (see below)		
Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched SEQUENCE DATABASES (see below) MEDLINE (see below)		
Electronic data base consulted during the international search (name of data base and, where practicable, search terms used) (as online, STN (DGENE): TGGG[AC] [AGT] [GC] T [AGT] AC [AG] GC [AGT] GC [AGT] CA [CT] TG AND GG [AGT] CA [CT] [AT] [GC] [ACT] GG [ACT] CC [ACT] [CT] T and SWISSPROT, GENBANK, EMBL, PIR: SEQ ID Nos: 6, 8 and 10 MEDLINE: 16p13.3 AND "serine protease"		
C. DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	Proc. Natl. Acad. Sci. USA 87, pages 960-3 (1990) Hanson, R.D. et al. "A cluster of hematopoietic serine protease genes is found on the same chromosomal band as the human α /S T-cell receptor locus." See whole document, especially page 961 column 2-962 column 1.	1,4,7,10,13,16,19,26, 27,31,32,35,38,46,49, 52,56,57,60,63
<input checked="" type="checkbox"/> Further documents are listed in the continuation of Box C <input type="checkbox"/> See patent family annex		
* Special categories of cited documents:		
"A" document defining the general state of the art which is not considered to be of particular relevance	"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention	
"E" earlier document but published on or after the international filing date	"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone	
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art	
"O" document referring to an oral disclosure, use, exhibition or other means	"&" document member of the same patent family	
"P" document published prior to the international filing date but later than the priority date claimed		
Date of the actual completion of the international search 31 March 1998	Date of mailing of the international search report 03 APR 1998	
Name and mailing address of the ISA/AU AUSTRALIAN PATENT OFFICE PO BOX 200 WODEN ACT 2606 AUSTRALIA Facsimile No.: (02) 6285 3929	Authorized officer JIM CHAN Telephone No.: (02) 6283 2340	

INTERNATIONAL SEARCH REPORT

International Application No.
PCT/AU 98/00085**Box I** Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☒ Claims Nos.: 19, 20, 26, 31, 44
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
the breadth of the claims was such that it was uneconomical to conduct a search that encompassed the full scope of the claims.
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a)

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International Application No.

PCT/AU 98/00085

C (Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	Proc. Natl. Acad. Sci. USA 87, pages 3811-5 (1990) Vanderslice, P. et al. "Human mast cell tryptase: multiple cDNAs and genes reveal a multigene serine protease family." See whole document	1-4,5-7,10-13,14-16,26-28,31,32-38,44,46-52,55-59,60-63
X	J. Reprod. Fertil. 100, pages 567-75 (1994) Bermudez, D. et al. "Proacrosin as a marker of meiotic and post-meiotic germ cell differentiation: quantitative assessment of human spermatogenesis with a monoclonal antibody." See whole document, in particular Introduction.	46-48, 50, 51, 55
X	J. Biol. Chem. 269(29) pages 18843-8 (1994) Yu, J.X. et al. "Prostasin is a novel human serine protease from seminal fluid." See whole document, in particular discussion.	1-3,5,6,10-12,14,15,27,28,31-34,37,44,46-48,50,51,55-59,61,62
X	J. Biol. Chem. 269 (31) pages 19976-82 (1994) Matsushima, M. et al. "Structural characterisation of porcine enteropeptidase." See whole document, especially figure 4.	1-3,5,6,10-12,14,15,27,28,31-34,37,44,46-48,50,51,55-59,61,62
X	J. Biol. Chem. 270 (22) pages 13483-89 (1995) Yu, J.X. et al. "Molecular cloning, tissue-specific expression, and cellular localisation of human prostasin mRNA." See whole document, especially figure 2, Introduction and Discussion.	1-3,5,6,10-12,14,15,27,28,31-34,36,37,41-43,44,46-48,50,51,55-59,61,62
X	Mol. Reprod. Dev. 43, pages 236-47 (1996) O'Brien, D.A. et al. "Boar proacrosin" expressed in spermatids of transgenic mice does not reach the acrosome and disrupts spermatogenesis." See whole document.	1-3,5,6,10-12,14,15,27,28,31-34,36,37,41-43,44,46-48,50,51,55-59,61,62